

FIG. 35

66-51021-01/0001/0002

EcoRI		
1	AATTCGAGCA GAAGCTGATC TCTGAGGAGG ATCTGTAGGG TGGTGGCTCT	
	TTAAGCTCGT CTTGCGACTAG AGACTCCTCC TAGACATCCC ACCACCGAGA	
51	GGTCCCGGTG ATTTTGATTA TGAAAAGATG GCAAACGCTA ATAAGGGGGC	
	CCAAGGCCAC TAAAACTAAT ACTTTCTAC CGTTGCGAT TATTCCCCCG	
101	TATGACCGAA AATGCCGATG AAAACGGCT ACAGTCTGAC GCTAAAGGCA	
	ATACTGGCTT TTACGGCTAC TTTTGCGCGA TGTCAGACTG CGATTCCCGT	
151	AACTTGATTG TGTCGCTACT GATTACGGTG CTGCTATCGA TGGTTTCATT	
	TTGAACCTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA	
201	GGTGACGTTT CCGGCCTTGC TAATGGTAAT GGTGCTACTG GTGATTTTGC	
	CCACTGCAAA GGCCGGAACG ATTACCATTA CCACGATGAC CACTAAAACG	
251	TGGCTCTAAT TCCCAAATGG CTCGAAGTCGG TGACGGTGAT AATTCACCTT	
	ACCGAGATTA AGGGTTTACC GAGTTCAGCC ACTGCCACTA TTAAGTGGAA	
XmnI		
301	TAATGAATAA TTTCGGTCAA TATTACCTT CCTCCCTCA ATCGGTTGAA	
	ATTACTTATT AAAGCAGTT ATAAATGGAA GGGAGGAGT TAGCCAACTT	

FIG. 35A-1

351	TGTCGCCCTT	TTGTCTTTGG	CGCTGGTAA	CCATATGAAT	TTTCTATTGA
	ACAGCGGGAA	AACAGAAACC	GCGACCATTT	GGTATACTTA	AAAGATAACT
401	TTGTGACAAA	ATAAACTTAT	TCCGTGGTGT	CTTTGCGTTT	CTTTTATATG
	AACACTGT	TATTTGAATA	AGGCACCACA	GAAACGCAAA	GAAAATATAC
451	TTGCCACCTT	TATGTATGTA	TTTTCTACGT	TTGCTAACAT	ACTGCCGTAAT
	AACGGTGGAA	ATACATACAT	AAAAGATGCA	AACGATTGTA	TGACGCATTA
HindIII					
501	AAGGAGTCTT	GATAAGCTTG	ACCTGTGAAG	TGAAAAATGG	CGCAGATTCT
	TTCCCTCAGAA	CTATTCGAAC	TGGACACTTC	ACTTTTACC	CGTCTAACA
PacI					
551	GCGACATTTT	TTTTGTCTGC	CGTTAATTA	AAGGGGGGGG	GGGGCCGGCC
	CGCTGTAAAA	AAACACAGACG	GCAAATTAAT	TTCCCCCCCC	CCCCGGCCGG
BsrGI					
601	TGGGGGGGGG	TGTACATGAA	ATTGTAACG	TTAATATTTT	GTAAAAATTC
	ACCCCCCCCC	ACATGTACTT	TAACA'TTTGC	AATTATAAAA	CAATTTTAAG

FIG. 35A-2

651	CGGTTAAATT	TTTGTTAAAT	CAGCTCATTT	TTTAACCAAT	AGGCCGAAAT
	CGCAATTAA	AAACAATTA	GTCGAGTAA	AAATTGGTTA	TCCGGCTTTA
701	CGGCAAAATC	CCTTATAAAT	CAAAAGAATA	GACCGAGATA	GGTTGAGTG
	GCCGTTTTAG	GGAATATTA	GTTTTCTTAT	CTGGCTCTAT	CCCAACTCAC
751	TTGTTCCAGT	TTGGAACAAG	AGTCCACTAT	TAAAGAACGT	GGACTCCAAC
	AACAAGGTCA	AACCTTGTC	TCAGGTGATA	ATTCTTGCA	CCTGAGGTTG
801	GTCAAAGGGC	GAAAACCGT	CTATCAGGC	GATGGCCAC	TACGAGAAC
	CAGTTTCCCG	CTTTTGGCA	GATAGTCCCG	CTACCGGGTG	ATGCTCTTGG
851	ATCACCCCTAA	TCAAGTTTTT	TGGGTCGAG	GTGCCGTAA	GCCTAAATC
	TAGTGGGATT	AGTTCAAAA	ACCCAGCTC	CACGGCATT	CGTGATTAG
BanII					
~~~~~					
901	GGAACCCCTAA	AGGGAGCCCC	CGATTTAGAG	CTTGACGGG	AAAGCCGGCG
	CCTTGGGATT	TCCCTCGGG	GCTAAATCTC	GAACTGCCCC	TTTCGGCCCG
951	AACGTGGCGA	GAAAGGAAGG	GAAGAAAGCG	AAAGGAGCGG	GCGCTAGGGC
	TTGCACCGCT	CTTTCCTTCC	CTTCTTTCGC	TTTCCTCGCC	CGCGATCCCG

FIG. 35A-3

1001 GCTGGCAAGT GTAGCGGTCA CGCTGGCGGT AACCACCACA CCCGCCGCCG  
CGACCGTTCA CATCGCCAGT GCGACGCGCA TTGGTGGTGT GGGCGGCGCG

NheI  
~~~~~

1051 TTAATGCGCC GCTACAGGC GCGTGCTAGC CATGTGAGCA AAAGGCCAGC
AATTACGCGG CGATGTCCCG CGCAGCATCG GTACACTCGT TTTCCGGTCG

1101 AAAAGGCCAG GAACCGTAA AAGGCCGCGT TGCTGGCGTT TTTCCATAGG
TTTTCCGGTC CTTGGCATT TTCCGGCGCA ACGACCGCAA AAAGGTATCC

1151 CTCGCGCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA GTCAGAGGTG
GAGCGGGGG GACTGCTCGT AGTGTTTTA GCTGCGAGTT CAGTCTCCAC

1201 GCGAAACCCG ACAGGACTAT AAAGATACCA GCGGTTTCCC CCTGGAAGCT
CGCTTTGGGC TGTCCTGATA TTTCTATGGT CCGCAAAGGG GGACCTTCGA

BssSI
~~~~~

1251 CCCTCGTGCG CTCTCCTGTT CCGACCCCTGC CGCTTACCGG ATACCTGTCC  
GGGAGCACGC GAGAGGACAA GGCTGGGACG GCGAATGGCC TATGGACAGG

1301 GCCTTTCTCC CTTGCGGAAG CGTGCGCGCT TCTCATAGCT CACGCTGTAG  
CGGAAAGAGG GAAGCCCTTC GCACCGCGAA AGAGTATCGA GTGCGACATC

FIG. 35A-4

1351 GTATCTCAGT TCGGTGTAGG TCGTTGCGCTC CAAGCTGGGC TGTGTGCACG  
CATAGAGTCA AGCCACATCC AGCAAGCGAG GTTCGACCCG ACACACGTGC

1401 AACCCCCCGT TCAGCCCGAC CGTGCGGCCT TATCCGGTAA CTATCGTCTT  
TTGGGGGCA AGTCGGGCTG GCGACGGGA ATAGGCCATT GATAGCAGAA

1451 GAGTCCAACC CGGTAAGACA CCACTTATCG CCACTGGCAG CAGCCACTGG  
CTCAGGTTGG GCCATTCTGT GCTGAATAGC GGTGACCGTC GTCGGTGACC

1501 TAACAGGATT AGCAGAGCGA GGTATGTAGG CCGTGCTACA GAGTTCTTGA  
ATTGTCCCTAA TCGTCTCGCT CCATACATCC GCCACGATGT CTCAGAAGACT

1551 AGTGGTGGCC TAACTACGGC TACACTAGAA GAACAGTATT TGGTATCTGC  
TCACCCACCG ATTGATGCCG ATGTGATCTT CTTGTCATAA ACCATAGACG

1601 GCTCTGCTGT AGCCAGTTAC CTTCCGAAAA AGAGTTGGTA GCTCTTGATC  
CGAGACGACA TCGGTCAATG GAAGCCTTTT TCTCAACCAT CGAGAACTAG

1651 CGGCAAAACAA ACCACCGCTG GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC  
GCCGTTTGTT TGGTGGCGAC CATCGCCACC AAAAACAACAA ACGTTCTGTCG

1701 AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCCTTT GATCTTTTCT  
TCTAATGCGC GTCTTTTTTT CCTAGAGTTC TTCTAGGAAA CTAGAAAAAGA

FIG. 35A-5

1751	ACGGGGTCTG	ACGCTCAGTG	GAACGAAAC	TCACGTTAAG	GGATTTTGGT
	TGCCCCCAGAC	TGCGAGTCAC	CTTGCTTTTG	AGTGCAATTC	CCTAAAAACCA
	BglII				
	~~~~~				
1801	CAGATCTAGC	ACCAGGCGTT	TAAGGGCAC	AATAACTGCC	TTAAAAAAT
	GTCTAGATCG	TGGTCCGCAA	ATTCCCCTGG	TTATTGACGG	AATTTTTTA
1851	TACGCCCCCG	CCTGCCACTC	ATCGCAGTAC	TGTTGTAATT	CATTAAGCAT
	ATGCGGGCG	GGACGGTGAG	TAGCGTCATG	ACAACATTAA	GTAATTTCGA
1901	TCTGCCGACA	TGGAAGCCAT	CACAAACGGC	ATGATGAACC	TGAATCGCCA
	AGACGGGCTGT	ACCTTCGGTA	GTGTTGCCC	TACTACTTGG	ACTTAGCGGT
1951	GCGGCATCAG	CACCTTGTCG	CCTTGCGTAT	AATATTTGCC	CATAGTGAAA
	CGCCGTAGTC	GTGGAACAGC	GGAACGCATA	TTATAAACGG	GTATCACTTT
2001	ACGGGGGCGA	AGAAGTTGTC	CATATTGGCT	ACGTTTAAAT	CAAAACTGGT
	TGCCCCCGCT	TCTTCAACAG	GTATAACCGA	TGCAAAATTA	GTTTGAACCA
2051	GAAACTCACC	CAGGGATTGG	CTGAGACGAA	AAACATATTC	TCAATAAACC
	CTTTGAGTGG	GTCCCTAACC	GACTCTGCTT	TTTGTATAAG	AGTTATTG

FIG. 35A-6

2101	CTTTAGGGAA ATAGGCCAGG TTTTCACCGT AACACGCCAC ATCTTGCGAA GAAATCCCTT TATCCGATCC AAAAGTGGCA TTGTGGGGTG TAGAACGCTT
2151	TATATGTGTA GAAACTGCCG GAAATCGTCG TGGTATTCAC TCCAGAGCGA ATATACACAT CTTTGACGGC CTTTAGCAGC ACCATAAGTG AGGTCTCGCT
2201	TGAAAAACGTT TCAGTTTGCT CATGGAAAAC GGTGTAACAA GGGTGAACAC ACTTTTGCAA AGTCAAACGA GTACCTTTTG CCACATTGTT CCCACTTG TG
2251	TATCCCATAT CACCAGCTCA CCGTCTTTCA TTGCCATACG GAAC TCCGGG ATAGGGTATA GTGGTCGAGT GGCAGAAAGT AACGGTATGC CTTGAGGCC
2301	TGAGCATTCA TCAGGCGGGC AAGAAATGTGA ATAAAGGCCG GATAAACTT ACTCGTAAGT AGTCCGCCCG TTCTTACACT TATTTCCGGC CTATTTTGAA
2351	GTGCTTATTT TTCTTTACGG TCTTTAAAAA GGCCGTAATA TCCAGCTGAA CACGAATAAA AAGAAATGCC AGAAATTTTT CCGGCATTAT AGGTCGACTT
2401	CGGTCTGGTT ATAGGTACAT TGAGCAACTG ACTGAAATGC CTCAAAAATGT GCCAGACCAA TATCCATGTA ACTCGTTGAC TGACTTTTACG GAGTTTTACA
2451	TCCTTACGAT GCCATTGGGA TATATCAACG GTGGTATATC CAGTGATTTT AGAAATGCTA CCGTAACCCT ATATAGTTGC CACCATATAG GTCACTAAAA

FIG. 35A-7

2501 TTTCTCCATT TTAGCTTCCT TAGCTCCTGA AAATCTCGAT AACTCAAAA
 AAAGAGGTAA AATCGAAGGA ATCGAGGACT TTAGAGCTA TTGAGTTTTT

2551 ATACGCCCGG TAGGATCTT ATTCATTAT GGTGAAAGTT GGAACCTCAC
 TATGCGGGCC ATCACTAGAA TAAAGTAATA CCACTTTCAA CCTGGGAGTG

AatII

~~~~~

2601 CCGACGTCTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC AGGCTTTACA  
 GGCTGCAGAT TACACTCAAT CGAGTGAGTA ATCCGTGGGG TCCGAAATGT

2651 CTTTATGCTT CCGGCTCGTA TGTGTGTGG AATTGTGAGC GGATAACAAT  
 GAAATACGAA GGCCGAGCAT ACAACACACC TTAACACTCG CCTATTGTTA

XbaI SphI

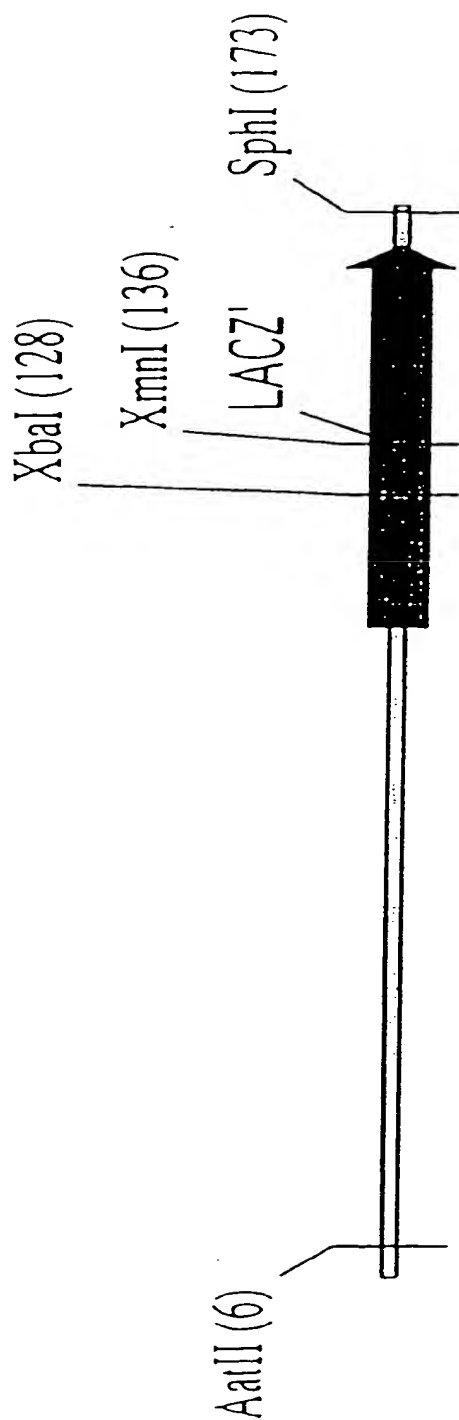
~~~~~

2701 TTCACACAGG AAACAGCTAT GACCATGATT ACGAATTCT AGAGCATGCC
 AAGTGTGTCC TTTGTGCGATA CTGGTACTAA TGCTTAAAGA TCTCGTACGC

EcoRI

2751 GGGG
 CCCC

FIG. 35A-8



M2

173 bp

FIG. 35A-9

M 2:

AatII

1 GACGTCCTTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC
CTGCAGAATT ACACTCAATC GAGTGAGTAA TCCGTGGGGT CCGAAATGTG

51 TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT
AAATACGAAG GCCGAGCATA CAACACACCT TAACACTCGC CTATTGTTAA

XmnI

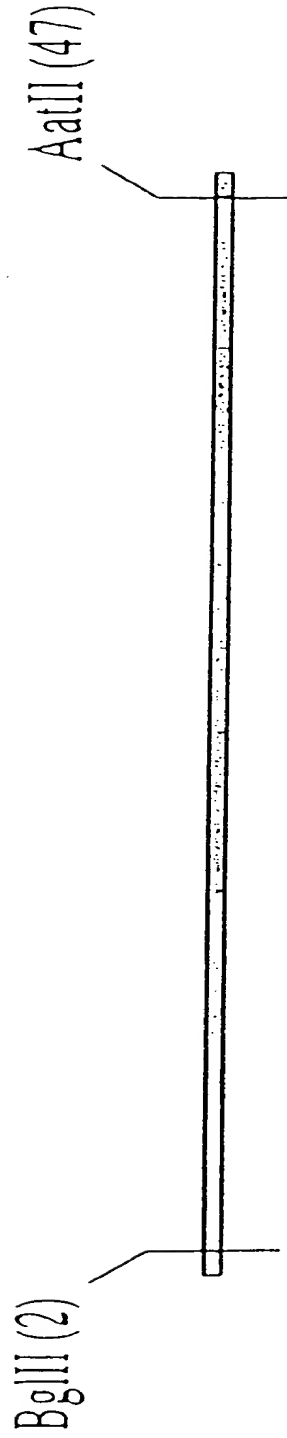
XbaI

101 TCACACAGGA AACAGCTATG ACCATGTCTA GAATAACTTC GTATAATGTA
AGTGTGTCCT TTGTCGATAC TGGTACAGAT CTTATTGAAG CATATTACAT

SphI

151 CGCTATACGA AGTTATCGCA TGC
GGGATATGCT TCAATAGCGT ACG

FIG. 35A-10



M3

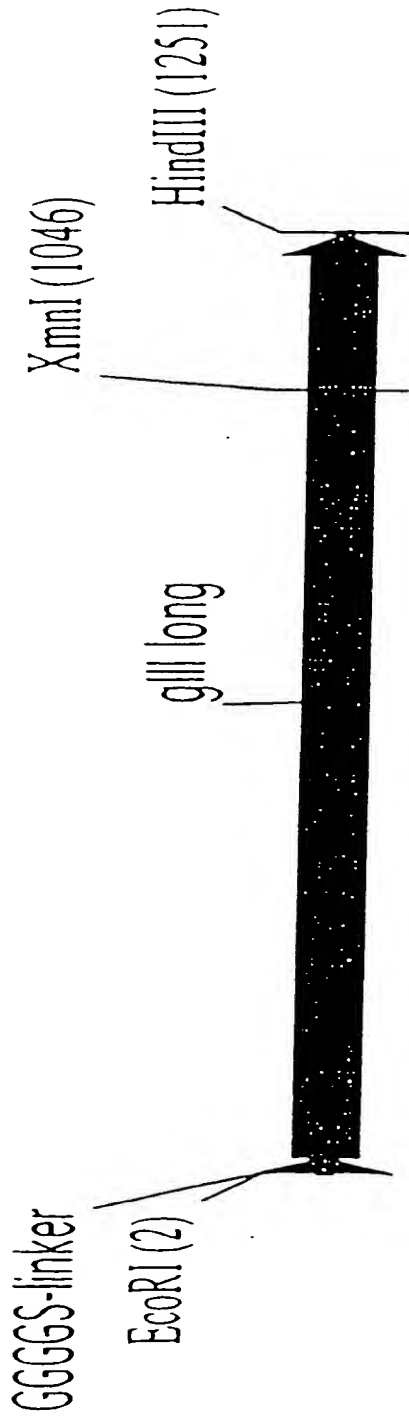
47 bp

FIG. 35A-11

M 3:

	BglII	AatII
	-----	-----
1	AGATCTCATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TGACGTC	
	TCTAGAGTAT TGAAGCATAT TACATACGAT ATGCTTCAAT ACTGCAG	

FIG. 35A-12



M7-I (long)

1255 bp

FIG. 35A-13

M 7-I (long):

ECORI

1	GAATTCGGTG	GTGGTGGATC	TGCGTGCGCT	GAAACGGTTG	AAAGTTGTTT
	CTTAAGCCAC	CACCACCTAG	ACGCACGCCA	CTTTGCCAAC	TTCAACAAA
51	AGCAAAATCC	CATACAGAAA	ATTCATTAC	TAACGTCTGG	AAAGACGACA
	TCGTTTTAGG	GTATGCTCTT	TAAGTAAATG	ATGCAGACC	TTTCTGCTGT
101	AAACTTTAGA	TCGTTACGCT	AACTATGAGG	GCTGTCTGTG	GAATGCTACA
	TTTGAATCT	AGCAATGCCA	TTGATACTCC	CGACAGACAC	CTTACGATGT
151	GGCGTTGTAG	TTTGTA CTGG	TGACGAAACT	CAGTGTTACG	GTACATGGGT
	CCGCAACATC	AAACATGACC	ACTGCTTTGA	GTCACAATGC	CATGTACCCA
201	TCCTATATGGG	CTTGCTATCC	CTGAAAATGA	GGGTGGTGGC	TCTGAGGGTG
	AGGATAACCC	GAACGATAGG	GACTTTTACT	CCCACCACCG	AGACTCCCAC
251	GCGGTTCTGA	GGGTGGCGGT	TCTGAGGGTG	GCGGTACTAA	ACCTCCTGAG
	CGCCAAGACT	CCCACCGCCA	AGACTCCCAC	CGCCATGATT	TGGAGGACTC
301	TACGGTGATA	CACCTATTCC	GGGCTATACT	TATATCAACC	CTCTCGACGG
	ATGCCACTAT	GTGGATAAGG	CCCGATATGA	ATATAGTTGG	GAGAGCTGCC

FIG. 35A-14

351 CACTTATCCG CCTGGTACTG AGCAAAACCC CGCTAATCCT AATCCTTCTC
GTGAATAGGC GGACCATGAC TCGTTTGGG GCGATTAGGA TTAGGAAGAG

401 TTGAGGAGTC TCAGCCTCTT AATACTTTCA TGTTTCAGAA TAATAGGTTC
AACTCCTCAG AGTCGGAGAA TTATGAAAGT ACAAGTCTT ATTATCCAAG

451 CGAAATAGGC AGGGGGCATT AACTGTTTAT ACGGGCACTG TTAACAAGG
GCTTTATCCG TCCCCCGTAA TTGACAAATA TGCCCCGTGAC AATGAGTTCC

501 CACTGACCCC GTTAAACTT ATTACCAGTA CACTCCTGTA TCATCAAAAG
GTGACTGGGG CAATTTTGAA TAATGGTCAT GTGAGGACAT AGTAGTTTC

551 CCATGTATGA CGCTTACTGG AACGGTAAAT TCAGAGACTG CGCTTTCCAT
GGTACATACT GCGAATGACC TTGCCATTGA AGTCTCTGAC GCGAAAGGTA

601 TCTGGCCTTA ATGAGGATTT ATTTGTTTGT GAATATCAAG GCCAATCGTC
AGACCGAAAT TACTCCTAAA TAAACAACA CTTATAGTTC CCGTTAGCAG

651 TGACCTGCCT CAACCTCCTG TCAATGCTGG CCGCGGCTCT GGTGGTGGTT
ACTGGACGGA GTTGGAGGAC AGTTACGACC GCCGCCGAGA CCACCACCAA

701 CTGGTGGCGG CTCTGAGGGT GGTGGCTCTG AGGGTGGCGG TTCTGAGGGT
GACCACCGCC GAGACTCCCA CCACCGAGAC TCCCACCGCC AAGACTCCCA

FIG. 35A-15

751	GGCGGCTCTG	AGGAGGCGG	TTCCGGTGGT	GGCTCTGGTT	CCGGTGATT
	CCGCCGAGAC	TCCCTCCGCC	AAGCCACCA	CCGAGACCAA	GGCCACTAAA
801	TGATTATGAA	AAGATGGCAA	ACGCTAATAA	GGGGGCTATG	ACCGAAAATG
	ACTAATACTT	TTCTACCGTT	TCCGATTATT	CCCCCGATAC	TGGCTTTTAC
851	CCGATGAAAA	CGCGCTACAG	TCTGACGCTA	AAGGCAAACT	TGATTCTGTC
	GGCTACTTTT	GCGCGATGTC	AGACTGCGAT	TTCCGTTTGA	ACTAAGACAG
901	GCTACTGATT	ACGGTGCTGC	TATCGATGGT	TTCATTGGTG	ACGTTTCCGG
	CGATGACTAA	TGCCACGACG	ATAGCTACCA	AAGTAACCAC	TGCAAAAGGCC
951	CCTTGCTAAT	GGTAATGGTG	CTACTGGTGA	TTTGTCTGGC	TCTAATTCCC
	GGAACGATTA	CCATTACCAC	GATGACCACT	AAAACGACCG	AGATTAAAGG
				XmnI	
1001	AAATGGCTCA	AGTCGGTGAA	GGTGATAATT	CACCTTTAAT	GAATAATTTC
	TTTACCGAGT	TCAGCCACTT	CCACTATTAA	GTGGAAATTA	CTTATTAAAG
1051	CGTCAATATT	TACCTTCCAT	CCCTCAATCG	GTTGAATGTC	GCCCTTTTGT
	GCAGTTATAA	ATGGAAGGTA	GGGAGTTAGC	CACTTACAG	CGGGAAAACA

FIG. 35A-16

```
1101 CTTTGGCGCT GGTAAACCCCT ATGAATTTTC TATTGATTGT GACAAATATA
    GAAACCGCGA CCATTGCGA TACTTAAAG ATAATAACA CTGTTTTATT

1151 ACTTATTCCG TGGTGTCCTT GCGTTCTTT TATATGTTGC CACCTTTATG
    TGAATAAGGC ACCACAGAAA CGCAAAGAAA ATATACAACG GTGGAAATAC

    HindIII

1201 TATGTATTTT CTACGTTTGC TAACATACTG CGTAATAAGG AGCTTTGATA
    ATACATAAAA GATGCAAACG ATTGTATGAC GCATTATTCC TCAGAACTAT

    HindI
    ---
1251 AGCTT
    TCGAA
```

FIG. 35A-17



M7-II (ss-TAG)

502 bp

FIG. 35A-18

M 7-II (ss-TAG) :

ECORI

1	CGGGAATTGG	GAGGCGGTTC	CGGTGGTGGC	TCTGGTTCCG	GTGATTTTGA
	GCCCTTAAGC	CTCCGCCAAG	GCCACCACCG	AGACCAAGGC	CACTAAAACT
51	TTATGAAAAG	ATGGCAAACG	CTAATAAGGG	GGCTATGACC	GAAAATGCCG
	AATACTTTTC	TACCGTTTGC	GATTATTCCC	CCGATACTGG	CTTTTACGGC
101	ATGAAAACGC	GCTACAGTCT	GACGCTAAAG	GCAAACCTGA	TTCTGTCCGT
	TACTTTTGCG	CGATGTCAGA	CTGCGATTTC	CGTTTGAAC	AAGACAGCGA
151	ACTGATTACG	GTGCTGCTAT	CGATGGTTTC	ATTGGTGACG	TTTCCGGCCT
	TGACTAATGC	CACGACGATA	GCTACCAAAG	TAACCACTGC	AAAGGCCGGA
201	TGCTAATGGT	AATGGTGCTA	CTGGTGATT	TGCTGGCTCT	AATCCCCAAA
	ACGATTACCA	TTACCAACGAT	GACCACTAAA	ACGACCGAGA	TTAAGGGTTT
251	TGGCTCAAGT	CGGTGACGGT	GATAATTAC	CTTTAATGAA	TAATTTCCGT
	ACCGAGTTCA	GCCACTGCCA	CTATTAAAGT	GAAATTACTT	ATTAAAGGCA

XmnI

FIG. 35A-19

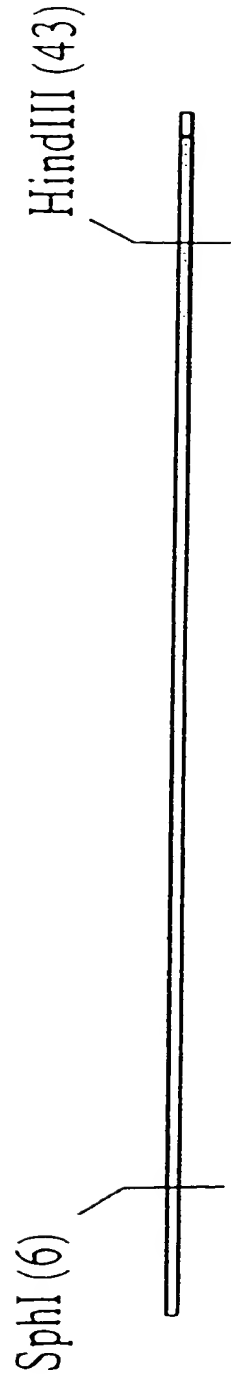
301 CAATATTAC CTTCCCTCCC TCAATCGGTT GAATGTCGCC CTTTGTCTT
GTTATAAATG GAAGGGAGGG AGTAGCCAA CTTACAGCGG GAAACAGAA
351 TGGCGCTGGT AAACCATATG AATTTCTAT TGATTGTGAC AAAATAAAT
ACCGCGACCA TTTGGTATAC TTAAGAAGATA ACTAACACTG TTTATTTGA
401 TATTCCTGG TGTCTTTGCG TTTCTTTTAT ATGTTGCCAC CTTTATGTAT
ATAAGGCACC ACAGAAACGC AAAGAAAATA TACAACGGTG GAAATACATA
451 GTATTTTCTA CGTTTGCTAA CATACTGCGT AATAAGGAGT CTTGATAAGC
CATAAAAGAT GCAAACGATT GTATGACGCA TTATTCCCTCA GAACTATTCC

HindIII

Hi
~
TT
AA

501

FIG. 35A-20



M8

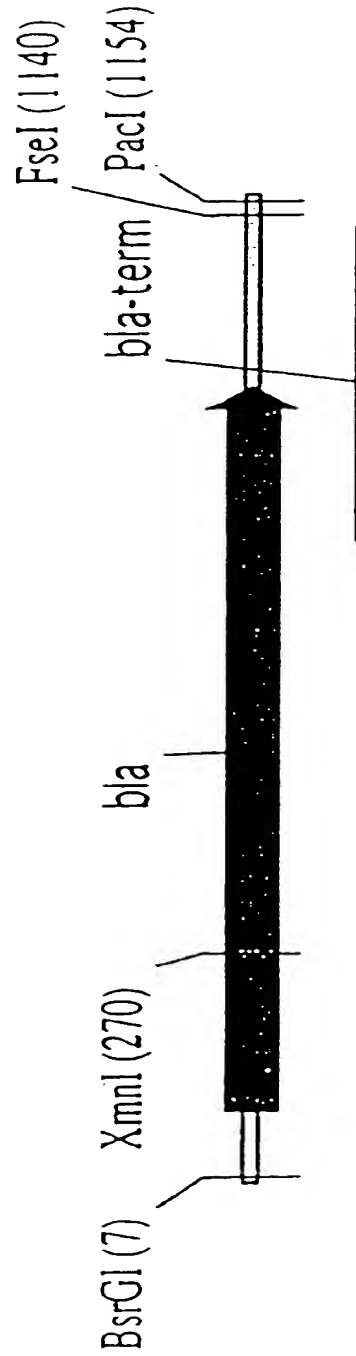
47 bp

FIG. 35A-21

M 8:

	SphI	HindIII
	-----	-----
1	GCATGCCATA ACTTCGTATA ATGTACGCTA TACGAAGTTA TAAGCTT	
	CGTACGGTAT TGAAGCATAT TACATGCCGAT ATGCTTCAAT ATTCGAA	

FIG. 35A-22



M10-II
1163 bp

FIG. 35A-23

M 10-II:

BsrGI

1	GGGGGTGTAC	ATTCAAATAT	GTATCCGCTC	ATGAGACAAT	AACCTGATA
	CCCCCACATG	TAAGTTTATA	CATAGGCGAG	TACTCTGTTA	TTGGGACTAT
51	AATGCTTCAA	TAATATTGAA	AAAGGAAGAG	TATGAGTATT	CAACATTTCC
	TTACGAAGTT	ATTATAACTT	TTTCCTTCTC	ATACTCATAA	GTTGTAAAGG
101	GTGTCGCCCT	TATCCCCTTT	TTTGCGGCAT	TTTGCCTTCC	TGTTTTTGCT
	CACAGCGGGA	ATAAGGGAAA	AAACGCCGTA	AAACGGAAGG	ACAAAACGA
151	CACCCAGAAA	CGCTGGTGAA	AGTAAAAGAT	GCTGAGGATC	AGTTGGGTGC
	GTGGGTCCTT	GCGACCACTT	TCATTTTCTA	CGACTCCTAG	TCAACCCACG
201	GCGAGTGGGT	TACATCGAAC	TGGATCTCAA	CAGCGGTAAG	ATCCTTGAGA
	CGCTCACCCA	ATGTAGCTTG	ACCTAGAGTT	GTCGCCATTC	TAGGAACTCT
251	GTTTTCGCCC	CGAAGAACGT	TTTCCAATGA	TGAGCACTTT	TAAAGTTCTG
	CAAAAGCGGG	GCTTCTTGCA	AAAGGTTACT	ACTCGTGAAA	ATTTCAGAGC

XmnI

FIG. 35A-24

301 CTATGTGGCG CCGTATTATC CCGTATTGAC GCCGGGCAAG AGCAACTCGG
GATACACCGC GCCATAATAG GGCATAACTG CGGCCCGTTC TCGTTGAGCC

351 TCGCCGCATA CACTATTCTC AGAATGACTT GGTGAGTAC TCACCAGTCA
AGCGGCGTAT GTGATAAGAG TCTTACTGAA CCAACTCATG AGTGGTCAGT

401 CAGAAAAGCA TCTTACGGAT GGCA TGACAG TAAAGAGAATT ATGCAGTGCT
GTCTTTTCGT AGAATGCCCTA CCGTACTGTC ATTCTCTTAA TACGTCACGA

451 GCCATAACCA TGAGTGATAA CACTGCGGCC AACTTACTTC TGACAACGAT
CGGTATTGGT ACTCACTATT GTGACGCCGG TTGAATGAAG ACTGTTGCTA

501 CGGAGGACCG AAGGAGCTAA CCGCTTTTTT GCACAACATG GGGATCATG
GCCTCCTGGC TTCCTCGATT GCGGAAAAAA CGTGTTGTAC CCCCTAGTAC

551 TAACTCGCCT TGATCGTTGG GAACCGGAGC TGAATGAAGC CATACCAAAC
ATTGAGCGGA ACTAGCAACC CTTGGCCCTCG ACTTACTCG GTATGGTTTG

601 GACGAGCGTG ACACCACGAT GCCTGTAGCA ATGGCAACAA CGTTGCGCAA
CTGCTCGCAC TGTGGTGCTA CCGACATCGT TACCGTTGTT GCAACGCGTT

651 ACTATTAACT GGCGAACTAC TTA CTCTAGC TTCCCGGCAA CAGTTAATAG
TGATAATTGA CCGCTTGATG AATGAGATCG AAGGCCGTT GTCAATTATC

FIG. 35A-25

701 ACTGGATGGA GCGGATAAAA GTGCAGGAC CACTTCTGCG CTCGGCCCTT
TGACCTACCT CCGCCTATTT CAACGTCCTG GTGAAGACGC GAGCCGGGAA

751 CCGGCTGGCT GGTTTATTGC TGATAAATCT GGAGCCGGTG AGCGTGGGTC
GGCCGACCGA CCAAATAACG ACTATTAGA CCTCGGCCAC TCGCACCCAG

801 TCGCGGTATC ATTGCAGCAC TGGGGCCAGA TGGTAAGCCC TCCCGTATCG
AGCGCCATAG TAACGTCGTG ACCCCGGTCT ACCATTTCGG AGGCATAGC

851 TAGTTATCTA CACGACGGGG AGTCAGGCAA CTATGGATGA ACGAAATAGA
ATCAATAGAT GTGCTGCCCC TCAGTCCGTT GATACCTACT TGCTTTATCT

901 CAGATCGCTG AGATAGGTGC CTCACTGATT AAGCATTTGG TAACTGTCAG
GTCTAGCGAC TCTATCCACG GAGTGACTAA TTCGTAACCC ATTGACAGTC

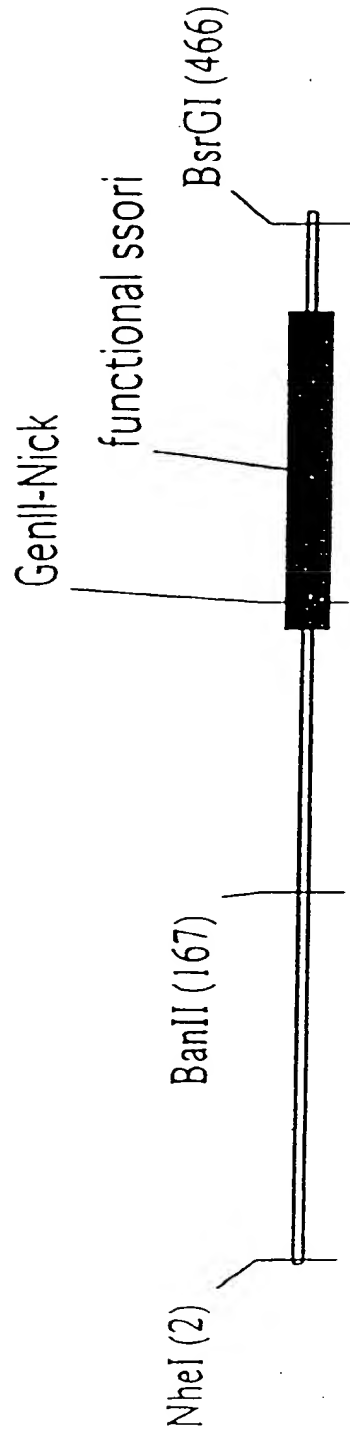
951 ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTTAA
TGGTTCAAAT GAGTATATAT GAAATCTAAC TAAATTTTGA AGTAAAAATT

1001 TTTAAAAGGA TCTAGGTGAA GATCCTTTT GATAATCTCA TGACCAAAT
AAATTTTCCT AGATCCACTT CTAGGAAAAA CTATTAGAGT ACTGGTTTTA

1051 CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAGA
GGGAATTGCA CTCAAAAGCA AGTGACTCG CAGTCTGGGG CATCTTTTCT

FIG. 35A-26

FIG. 35A-27



M11-II

470 bp

FIG. 35A-28

M11-II:

NheI

```

1  GCTAGCACGC GCCCTGTAGC GCGGCATTAA GCGCGGCGGG TGTGGTGGTT
   CGATCGTGCG CGGACATCG CCGGTAATT CCGCGCGCCC ACACCACCAA

51  ACGCGCAGCG TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT
   TGCGCGTCGC ACTGGGATG TGAACGGTCG CGGATCGCG GCGAGGAAA

101 CGCTTTCCTC CCTTCCTTTC TCGCCACGTT CCGCGGCTTT CCCCGTCAAG
   GCGAAAGAAG GGAAGGAAAG AGCGGTGCAA GCGGCCGAAA GGGCAGTTC
  
```

BanII

```

151 CTCATAAATCG GGGGCTCCCT TTAGGGTTCC GATTAGTGC TTTACGGCAC
   GAGATTTAGC CCCCAGGGA AATCCCAAGG CTAATCAGG AAATGCCGTG

201 CTCGACCCCA AAAAATTGA TTAGGGTGAT GGTTCTCGTA GTGGGCCATC
   GAGCTGGGGT TTTTGAAC TATCCCACTA CCAAGAGCAT CACCCGGTAG

251 GCCCTGATAG ACGGTTTTC GCCCTTTGAC GTTGAGTCC ACGTTCCTTA
   CCGGACTATC TGCCAAAAAG CCGGAAACTG CAACCTCAGG TGCAGAAAT
  
```

FIG. 35A-29

```
301  ATAGTGGACT CTTGTTCCAA ACTGGAACAA CACTCAACCC TATCTCGGTC
    TATCACCTGA GAACAAGGTT TGACCTTGTT GTGAGTTGGG ATAGAGCCAG

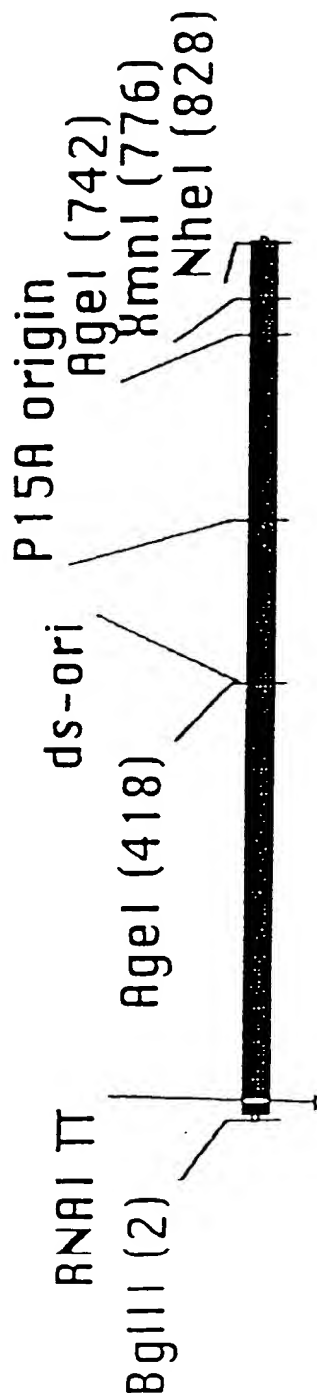
351  TATTCTTTTG ATTTATAAGG GATTTTGCCG ATTTCCGGCCT ATTGGTTAAA
    ATAAGAAAAC TAAATATTCC CTAAACGGC TAAAGCCGGA TAACCAATTT

401  AAATGAGCTG ATTTAACAAA AATTAAACGC GAATTTTAAC AAAATATTAA
    TTACTCGAC TAAATTGTTT TTAAATTGCG CTTAAAAATTG TTTTATAATT

          BsrGI
          -----

451  CGTTTACAAT TTCATGTACA
    GCAAATGTTA AAGTACATGT
```

FIG. 35A-30



M12

832 bp

FIG. 35A-31

M 12:

BglII

~~~~~

|     |            |            |            |             |             |
|-----|------------|------------|------------|-------------|-------------|
| 1   | AGATCTAATA | AGATGATCTT | CTTGAGATCG | TTTTGGTCTG  | CGCGTAATCT  |
|     | TCTAGATTAT | TCTACTAGAA | GAACCTTAGC | AAAACCCAGAC | GCGCATTAGA  |
| 51  | CTTGCTCTGA | AAACGAAAAA | ACCGCCTTGC | AGGGCGGTTT  | TTCGTAGGTT  |
|     | GAACGAGACT | TTTGCTTTTT | TGGCGGAACG | TCCCGCCAAA  | AAGCATCCAA  |
| 101 | CTCTGAGCTA | CCAACTCTTT | GAACCGAGGT | AACTGGCTTG  | GAGGAGCGCA  |
|     | GAGACTCGAT | GGTTGAGAAA | CTTGGCTCCA | TTGACCGAAC  | CTCCTCGCGT  |
| 151 | GTCACTAAAA | CTTGTCCTTT | CAGTTTAGCC | TTAACC GGCG | CATGACTTCA  |
|     | CAGTGATTTT | GAACAGGAAA | GTCAAATCGG | AATTGGCCCG  | GTA CTGAAGT |
| 201 | AGACTAACTC | CTCTAAATCA | ATTACCAGTG | GCTGCTGCCA  | GTGGTGCTTT  |
|     | TCTGATTGAG | GAGATTTAGT | TAATGGTCAC | CGACGACGGT  | CACCA CGAAA |
| 251 | TGCATGTCTT | TCCGGGTTGG | ACTCAAGACG | ATAGTTACCG  | GATAAGGCGC  |
|     | ACGTACAGAA | AGGCCCCAAC | TGAGTTCTGC | TATCAATGGC  | CTATTCCGCG  |
| 301 | AGCGGTCGGA | CTGAACGGGG | GGTTCGTGCA | TACAGTCCAG  | CTTGGAGCGA  |
|     | TCGCCAGCCT | GACTTGCCCC | CCAAGCACGT | ATGTCAGGTC  | GAACCTCGCT  |

FIG. 35A-32

351 ACTGCCCTACC CGGAAGTGAAG TGTACGGCGT GGAATGAGAC AAACGGGGCC  
TGACGGGATGG GCCTTGACTC ACAGTCCGCA CCTTACTCTG TTGCGCGCGG

AgeI  
-----

401 ATAACAGCGG AATGACACCG GTAACCGAA AGGCAGGAAC AGGAGAGCGC  
TATTGTGCGC TTAAGTGGC CATTGGCTT TCCGTCCCTG TCCTCTCGCG

451 AGGAGGGAGC CGCCAGGGGG AAACGCCCTGG TATCTTTATA GTCCTGTCCG  
TCCTCCCTCG GCGGTCCCCC TTGCGGAGC ATAGAAATAT CAGGACAGCC

501 GTTTCGCCAC CACTGATTG AGCGTCAGAT TTCGTGATGC TTGTCAGGGG  
CAAAGCGGTG GTGACTAAAC TCGCAGTCTA AAGCACTACG AACAGTCCCC

551 GGCGGAGCCT ATGGAAGAAC GGCCTTGCCG CGGCCCTCTC ACTTCCCTGT  
CCGCCCTCGA TACCTTTTG CCGAAACGGC GCCGGGAGAG TGAAGGGACA

601 TAAGTATCTT CCTGGCATCT TCCAGGAAAT CTCCGCCCCG TTCGTAAGCC  
ATTCATAGAA GGACCGTAGA AGTCCCTTTA GAGCGGGGC AACATTCCG

651 ATTTCCGCTC GCCGCAGTCG AACGACCGAG CGTAGCGAGT CAGTGAGCGA  
TAAAGGCGAG CCGCGTCAGC TTGCTGGCTC GCATCGCTCA GTCACCTCGT

FIG. 35A-33

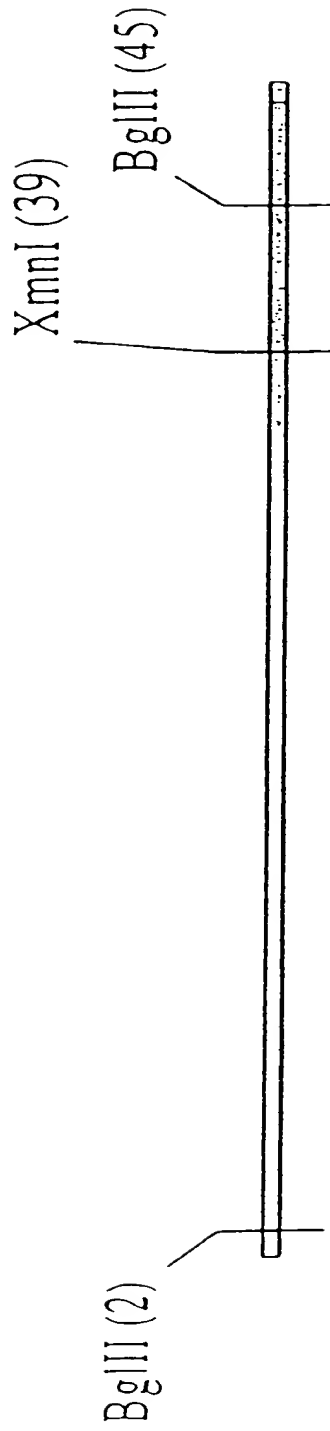
```

701  GGAAGCGGAA  TATATCCTGT  ATCACATATT  CTGCTGACGC  CTGCTGACGC  ACCGGTGCAG
      CCTTCGCCCTT  ATATAGGACA  TAGTGTATAA  GACGACTGCG  TGGCCACGTC
      AgeI
      ~~~~~

751 CCTTTTTTCT CCTGCCACAT GAAGCACTTC ACTGACACCC TCATCAGTGC
 GGAAAAAAGA GGACGGTGTA CTTCGTGAAG TGA CTGTGGG AGTAGTCACG
 XmnI
      ~~~~~

801  CAACATAGTA  AGCCAGTATA  CACTCCGCTA  GC
      GTTGATATCAT  TCGGTCATAT  GTGAGGCGAT  CG
      NheI
      ~~~~~
```

FIG. 35A-34



M13

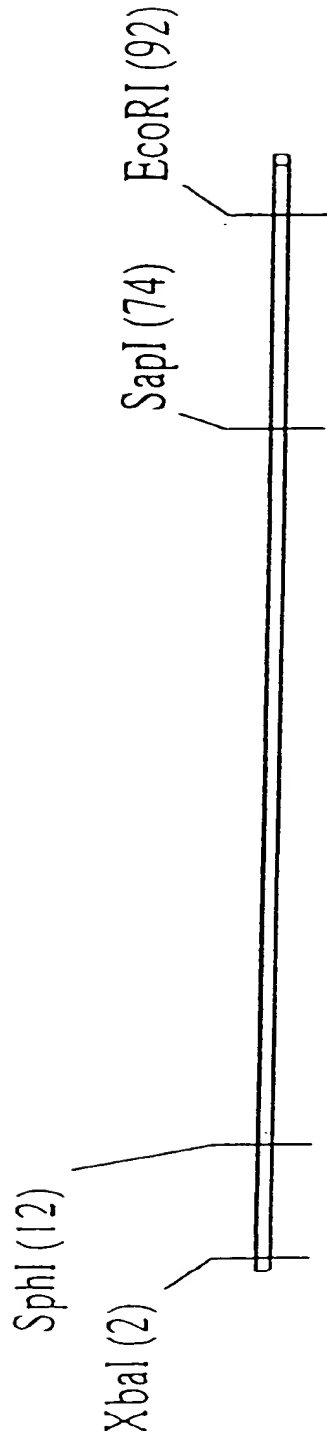
49 bp

FIG. 35A-35

M 13:

|   | BglII                                                 | XmnI  | BglII |
|---|-------------------------------------------------------|-------|-------|
| 1 | AGATCTCATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TTCAGATCT | ----- | ----- |
|   | TCTAGAGTAT TGAAGCATAT TACATACGAT ATGCTTCAAT AAGTCTAGA |       |       |

FIG. 35A-36



M19

96 bp

FIG. 35A-37

M 19:

```

XbaI SphI

1 TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAGCA CTATTGCACT
 AGATCTCGTA CGCATCCTCT TTTATTTTAC TTGTTTCGT GATAACGTGA

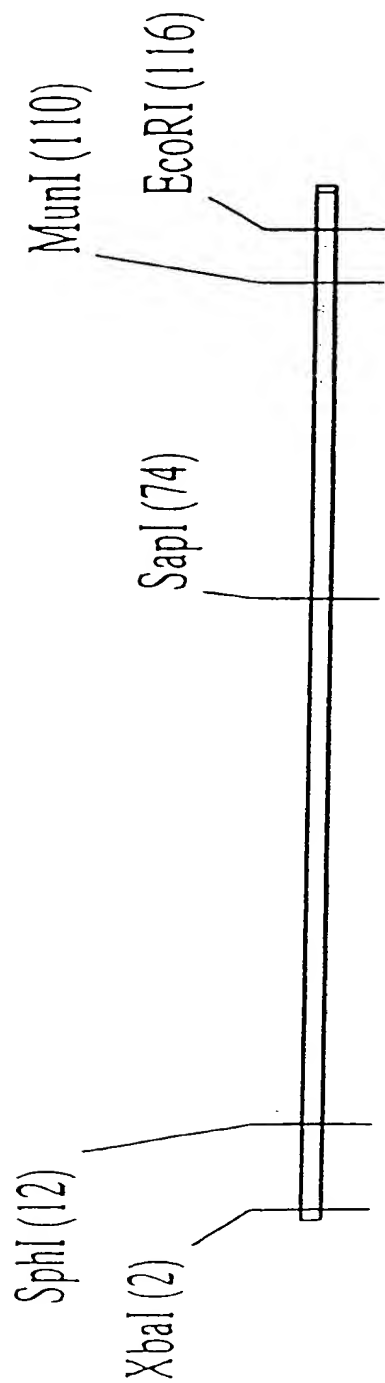
SapI

51 GGCACCTCTTA CCGTTGCTCT TCACCCCTGT TACCAAGCC GAATTC
 CCGTGAGAAAT GGCAACGAGA AGTGGGACA ATGGTTTCGG CTTAAG

EcoRI

```

FIG. 35A-38



M20

120 bp

FIG. 35A-39



M 20:

```

XbaI SphI

1 TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT
 AGATCTCGTA CGCATCCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

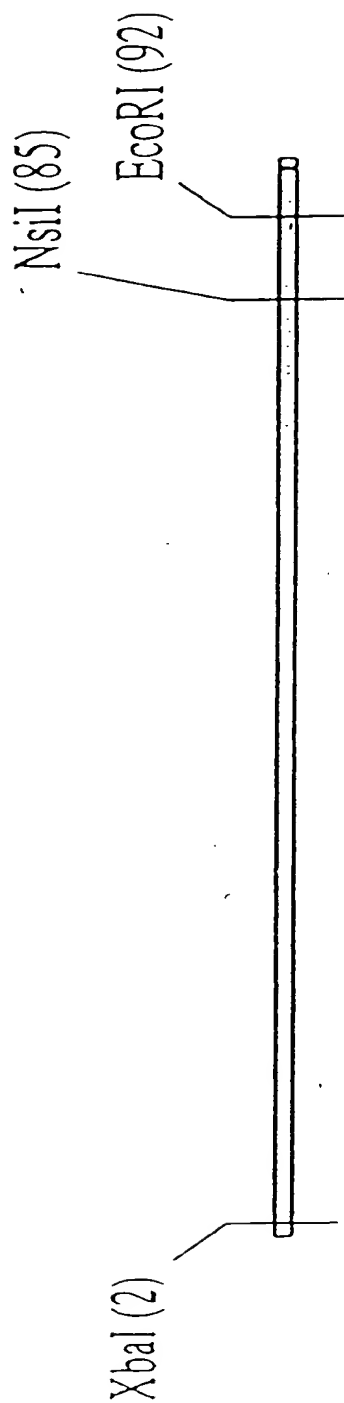
SapI

51 GGCACCTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG
 CCGTGAGAAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC

MunI EcoRI

101 ATGAAGTGCA ATTGGAATTC
 TACTTCACGT TAACCTTAAG
```

FIG. 35A-40



M21

96 bp

FIG. 35A-41

M 21:

XbaI

-----

1 TCTAGAGGTT GAGGTGATT TATGAAAAAG AATATCGCAT TTCTTCTTGC  
AGATCTCCAA CTCCACTAAA ATACTTTTC TTATAGCGTA AAGAAGAACG

NsiI

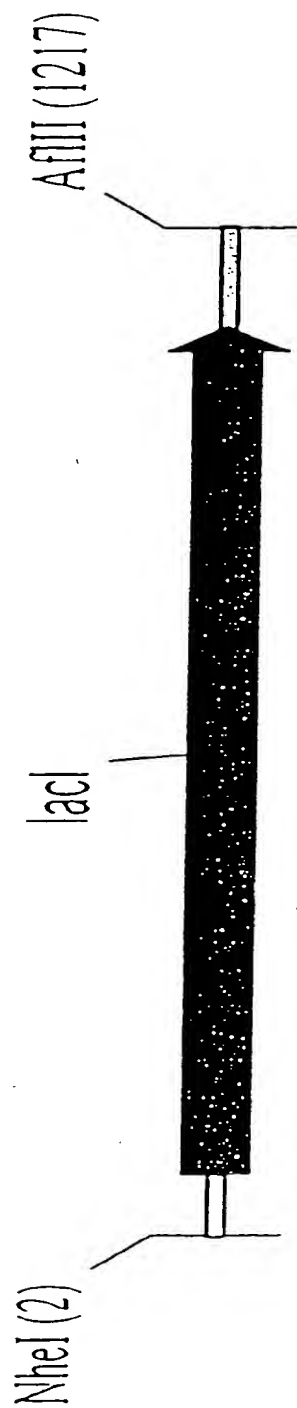
-----

EcoRI

-----

51 ATCTATGTTT GTTTTCTTCTA TTGCTACAAA TGCATACGCT GAATTC  
TAGATACAAG CAAAAAAGAT AACGATGTTT ACGTATGCCA CTTAAG

FIG. 35A-42



M41

1221 bp

FIG. 35A-43

M 41:

NheI

-----

|     |             |             |             |            |             |
|-----|-------------|-------------|-------------|------------|-------------|
| 1   | GCTAGCATCG  | AATGGCGCAA  | AACCTTTTCG  | GGTATGGCAT | GATAGCGCCC  |
|     | CGATCGTAGC  | TTACCCGCGTT | TTGGAAAGCG  | CCATACCGTA | CTATCGCGGG  |
| 51  | GGAAGAGAGT  | CAATTCAGGG  | TGGTGAATGT  | GAAACCAGTA | ACGTTATACG  |
|     | CCTTCTCTCA  | GTTAAGTCCC  | ACCACTTACA  | CTTTGGTCAT | TGCAATATGC  |
| 101 | ATGTCGCAGA  | GTATGCCGGT  | GTCTCTTATC  | AGACCGTTTC | CCGCGTGGTG  |
|     | TACAGCGTCT  | CATACGGCCA  | CAGAGAAATAG | TCTGGCAAAG | GGCGCACCCAC |
| 151 | AACCAGGCCA  | GCCACGTTTC  | TGCGAAACG   | CGGGAATAAG | TGGAAGCGGC  |
|     | TTGGTCCGGT  | CGGTGCAAAG  | ACGCTTTTGC  | GCCCTTTTTC | ACCTTCGCCC  |
| 201 | GATGGCGGAG  | CTGAATTACA  | TTCCTAACCG  | CGTGGCACAA | CAACTGGCGG  |
|     | CTACCGCCTC  | GACTTAATGT  | AAGGATTGGC  | GCACCGTGTT | GTTGACCGCC  |
| 251 | GCAAAACAGTC | GTGCTGATT   | GGCGTTGCCA  | CCTCCAGTCT | GGCCCTGCAC  |
|     | CGTTTGTCAG  | CAACGACTAA  | CCGCCAACGGT | GGAGGTCAGA | CCGGGACGTG  |
| 301 | GGCCCGTCGC  | AAATTGTGCG  | GGCGATTAAA  | TCTCGCGCCG | ATCAACTGGG  |
|     | CGCGGCAGCG  | TTTAACAGCG  | CCGCTAATTT  | AGAGCGCGGC | TAGTTGACCC  |

FIG. 35A-44

351 TCCAGCGTG GTCGTGTCGA TGGTAGAAGC AAGCGGCGTC GAAGCCTGTA  
ACGGTCGCAC CAGCACAGCT ACCATCTTGC TTCGCCGCAG CTCGGACAT

401 AAGCGGCGGT GCACAACTCTT CTCGCGCAAC GTGTCAGTGG GCTGATTATT  
TTCGCCGCCA CGTGTTAGAA GAGCGCGTTG CACAGTCACC CGACTAATAA

451 AACTATCCGC TGGATGACCA GGATGCTATT GCTGTGGAAG CTGCCCTGCAC  
TTGATAGGCG ACCTACTGGT CCTACGATAA CGACACCTTC GACGGACGTG

501 TAATGTTCGG GCGTTATTTC TTGATGTCTC TGACCAGACA CCCATCAACA  
ATTACAAGGC CGCAATAAAG AACTACAGAG ACTGGTCTGT GGGTAGTTGT

551 GTATTATTTT CTCCCATGAG GACGGTACGC GACTGGGCGT GGAGCATCTG  
CATAATAAAA GAGGGTACTC CTGCCATGCG CTGACCCGCA CCTCGTAGAC

601 GTCGCATTGG GCCACCAGCA AATCGCGCTG TTAGCTGGCC CATTAGTTC  
CAGCGTAACC CGGTGGTCGT TTAGCGCGAC AATCGACCGG GTAATTCAAG

651 TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAAATAT CTCACTCGCA  
ACAGAGCCGC GCAGACGCAG ACCGACCGAC CGTATTTATA GAGTGAGCGT

701 ATCAAATTCA GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC  
TAGTTTAAAGT CCGCTATCGC CTTGCCCTTC CGCTGACCTC ACGGTACAGG

FIG. 35A-45

751 GGTTTTCAAC AAACCATGCA AATGCTGAAT GAGGGCATCG TTCCCACGTC  
CCAAAAGTTG TTTGGTACGT TTACGACTTA CTCCCCTAGC AAGGGTGACG

801 GATGCTGGTT GCCAACGATC AGATGGCCGCT GGGCGCAATG CGTGCCATTA  
CTACGACCAA CGGTTGCTAG TCTACCGCGA CCCGCGTTAC GCACGGTAAT

851 CCGAGTCCGG GCTGCCGGTT GTGCCGGACA TCTCGGTAGT GGGATACGAC  
GGCTCAGGCC CGACGCGCAA CCACGCCCTGT AGAGCCATCA CCTATGCTG

901 GATACCGAGG ACAGCTCATG TTATATCCCG CCGCTGACCA CCATCAAACA  
CTATGGCTCC TGTCGAGTAC AATATAGGC GCGACTGGT GGTAGTTTGT

951 GGATTTTCGC CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT  
CCTAAAAGCG GACGACCCCG TTTGGTCGCA CTTGGCGAAC GACGTTGAGA

1001 CTCAGGGCCA GCGGTGAAG GGCAATCAGC TGTGCCCCGT CTCACTGGTG  
GAGTCCCCGT CCGCCACTTC CCGTTAGTCG ACAACGGGCA GAGTGACCAC

1051 AAAAGAAAAA CCACCCCTGGC TCCCAATACG CAAACCGCCT CTCCCCGCGC  
TTTTCTTTT GTGGGACCG AGGGTTATGC GTTTGGCGGA GAGGGGCGCG

1101 GTTGGCCGAT TCACTGATGC AGCTGGCAGC ACAGGTTTCC CGACTGGAAA  
CAACCGGCTA AGTGACTACG TCGACCGTGC TGTCCAAGG GCTGACCTTT

FIG. 35A-46

1151 GCGGGCAGTG AGGCTACCCG ATAAAAGCGG CTTCCTGACA GGAGGCCGTT  
CGCCCGTCAC TCCGATGGGC TATTTTCGCC GAAGGACTGT CCTCCGGCAA

AflII

-----

1201 TTGTTTGGCA GCCCACTTAA G  
AACAAACGT CCGGTGAATT C

FIG. 35A-47



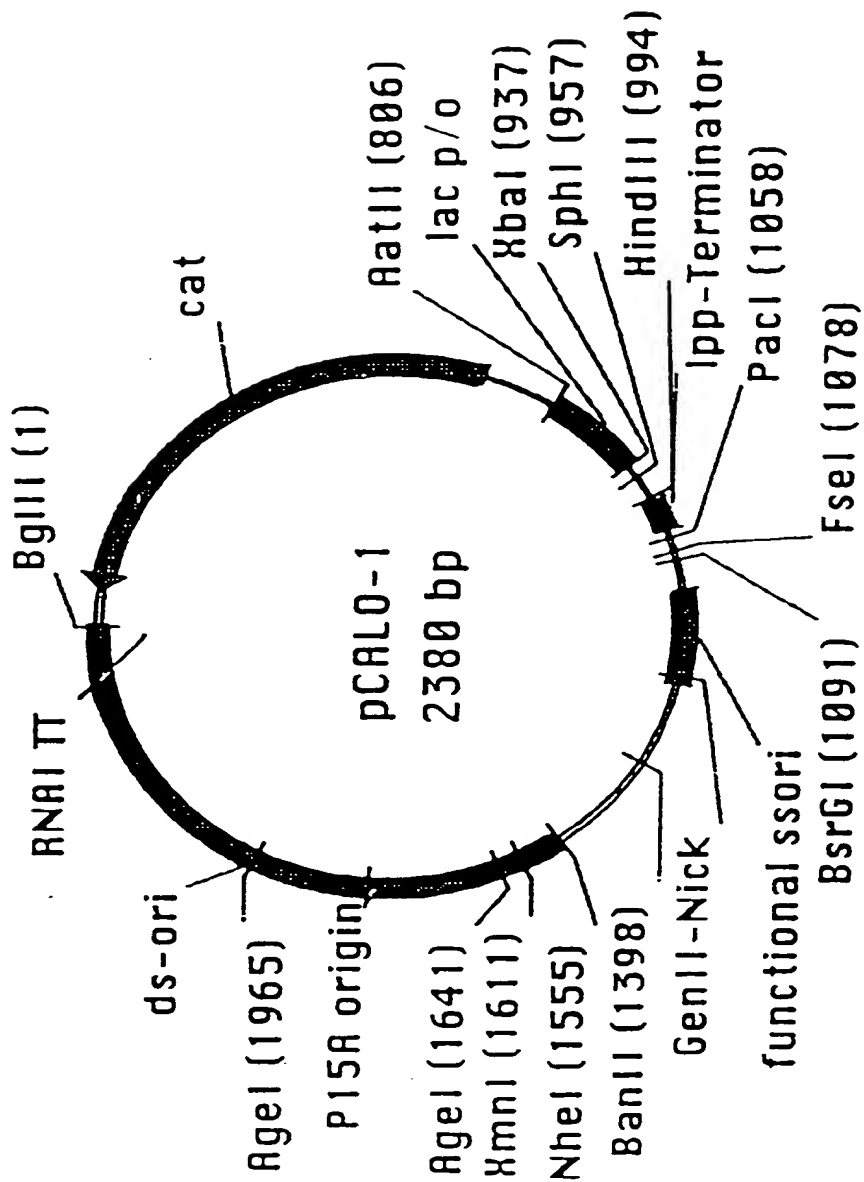


FIG. 35A-48

pCALO-1:  
Bg1II  
~~~~~  
1 GATCTAGCAC CAGGCGTTTA AGGCACCAA TAACTGCCTT AAAAAAATTA  
CTAGATCGTG GTCCGCAAAAT TCCCGTGGTT ATGACGGAA TTTTTTTAAAT  
  
51 CGCCCCGCC TGCCTCTCAT CGCAGTACTG TTGTAATTCA TTAAGCATTC  
GCGGGCGGG ACGGTGAGTA GCGTCATGAC AACATTAACT AATTCTAAG  
  
101 TGCCGACATG GAAGCCATCA CAAACGGCAT GATGAACCTG AATCGCCAGC  
ACGGCTGTAC CTTGGGTAGT GTTTGCCGTA CTAATTGGAC TTAGCGGTCTG  
  
151 GGCATCAGCA CCTTGTCGCC TTGCGTATAA TATTTGCCCA TAGTGAAAC  
CCGTAGTCGT GGAACAGCGG AACGCATATT ATAAACGGGT ATCACTTTTG  
  
201 GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA AAACCTGGTGA  
CCCCCGCTTC TTCAACAGGT ATAACCGATG CAAATTAGT TTTGACCACT  
  
251 AACTCACCCA GGGATTGGCT GAGACGAAA ACATATTCTC AATAAACCCCT  
TTGAGTGGGT CCTAACCGA CTCGTCTTT TGTATAAGAG TTATTTGGGA  
  
301 TTAGGGAAAT AGGCCAGGTT TTCACCGTAA CACGCCACAT CTTGCCAATA  
AATCCCTTTA TCCGGTCCAA AAGTGGCATT GTGCGGTGTA GAACGCTTAT

FIG. 35A-49

351	TATGTGTAGA	AAC TGCCGGA	AATCGTCGTG	GTAT TCACTC	CAGAGCGATG
	ATACACATCT	TTGACGGCCT	TTAGCAGCAC	CATAAGTGAG	GTCTCGCTAC
401	AAAACGTTTC	AGTTTGCTCA	TGGA AAACGG	TGTAACAAGG	GTGAACACTA
	TTTTGCAAAG	TCAAACGAGT	ACCTTTTGCC	ACATTGTTCC	CACTTG TGAT
451	TCCCATATCA	CCAGCTCACC	GTCTTTTCATT	GCCATACGGA	ACTCCGGGTG
	AGGGTATAGT	GGTCGAGTGG	CAGAAAGTAA	CGGTATGCCT	TGAGGCCCCAC
501	AGCATTTCATC	AGGCGGGCAA	GAATGTGAAT	AAAGGCCCGA	TAAAACTTGT
	TCGTAAGTAG	TCCGCCCGTT	CTTACACTTA	TTCCGGGCCT	ATTTTGAACA
551	GCTTATTTTT	CTTTACGGTC	TTTAAAAGG	CCGTAATATC	CAGCTGAACG
	CGAATAAAAA	GAAATGCCAG	AAATTTTTC	GGCATTTATAG	GTCGACTTGC
601	GTCTGGTTAT	AGGTACATTG	AGCAACTGAC	TGAAATGCCT	CAAAATGTTT
	CAGACCAATA	TCCATGTAAC	TCGTTGACTG	ACTTTACGGA	GTTT TACAAG
651	TTTACGATGC	CATTGGGATA	TATCAACGGT	GGTATATCCA	GTGATTTT T
	AAATGCTACG	GTAACCCCTAT	ATAGTTGCCA	CCATATAGGT	CACTAAAAAA
701	TCTCCATTTT	AGCTTCCCTTA	GCTCCTGAAA	ATCTCGATAA	CTCAAAAAAT
	AGAGGTAAAA	TCGAAGGAAT	CGAGGACTTT	TAGAGCTATT	GAGTTTTTTA

FIG. 35A-50

751	ACGCCCCGGTA	GTGATCTTAT	TTCAATTATGG	TGAAAGTTGG	AACCTCACCC
	TGCGGGCCAT	CACTAGAAATA	AAGTAATACC	ACTTTCAACC	TTGGAGTGCG
	AatII				
	~~~~~				
801	GACGTCTAAT	GTGAGTTAGC	TCACTCATTA	GGCACCCAG	GCTTTACACT
	CTGCAGATTA	CACTCAATCG	AGTGAGTAAT	CCGTGGGGTC	CGAAATGTGA
851	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	TTGTGAGCGG	ATAACAATTT
	AATACGAAGG	CCGAGCATAC	AACACACCTT	AACACTCGCC	TATTGTTAAA
	XbaI				
	~~~~~				
901	CACACAGGAA	ACAGCTATGA	CCATGATTAC	GAATTTCTAG	ACCCCCCCCC
	GTGTGTCCTT	TGTCGATACT	GGTACTAATG	CTTAAAGATC	TGGGGGGGGG
	SphI				
	~~~~~				
951	CGCATGCCAT	AACTTCGTAT	AATGTACGCT	ATACGAAGTT	ATAAGCTTGA
	GGGTACGGTA	TTGAAGCATA	TTACATGCCA	TATGCTTCAA	TATTCGAAC
1001	CCTGTGAAGT	GAAAAATGGC	GCAGATTGTG	CGACATTTT	TTTGTCTGCC
	GGACACTTCA	CTTTTACCG	CGTCTAACAC	GCTGTAAAAA	AAACAGACGG

FIG. 35A-51

	PacI	FseI	BsrGI
1051	~~~~~ GTTTAATTAA AGGGGGGGGG GGGCCGGCCT GGGGGGGGT GTACATGAAA CAAAATTAATT TCCCCCCCCC CCGGCCCGGA CCCCCCCCCA CATGTACTTT	~~~~~ GGGGGGGGGG GGGCCGGCCT GGGGGGGGT GTACATGAAA CAAAATTAATT TCCCCCCCCC CCGGCCCGGA CCCCCCCCCA CATGTACTTT	~~~~~ GGGGGGGGGG GGGCCGGCCT GGGGGGGGT GTACATGAAA CAAAATTAATT TCCCCCCCCC CCGGCCCGGA CCCCCCCCCA CATGTACTTT
1101	TTGTAAACGT TAATATTTTG TTAATAATTCG CGTTAAATTT TTGTTAAATC AACATTTGCA ATTATAAAAC AATTTTAAGC GCAATTAA AACAATTAG	TTAATAATTCG CGTTAAATTT TTGTTAAATC AACATTTGCA AATTTTAAGC GCAATTAA AACAATTAG	CGTTAAATTT TTGTTAAATC GCAATTAA AACAATTAG
1151	ACCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC CTTATAAATC TCGAGTAAAA AATTGGTTAT CCGGCTTTAG CCGTTTTAGG GAATATTTAG	GGCCGAAATC GGCAAAATCC CTTATAAATC AATTGGTTAT CCGGCTTTAG CCGTTTTAGG GAATATTTAG	GGCAAAATCC CTTATAAATC CGTTTTTAGG GAATATTTAG
1201	AAAAGAATAG ACCGAGATAG GGTGAGTGT TGTTCAGTT TGGAAACAAGA TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA ACCTTGTTCT	GGTGAGTGT TGTTCAGTT TGGAAACAAGA TGTTCAGTT TGTTCAGTT TGGAAACAAGA	TGTTCAGTT TGGAAACAAGA ACAAGGTCAA ACCTTGTTCT
1251	GTCCACTATT AAAGAACGTG GACTCCAACG TCAAAGGGCG AAAAACCGTC CAGGTGATAA TTTCTTGCAC CTGAGGTTGC AGTTTCCCGC TTTTGTGGCAG	GACTCCAACG TCAAAGGGCG TCAAAGGGCG CTGAGGTTGC AGTTTCCCGC TCAAAGGGCG	TCAAAGGGCG AAAAACCGTC AGTTTCCCGC TTTTGTGGCAG
1301	TATCAGGGCG ATGGCCCCACT ACGAGAACCA TCACCCCTAAT CAAGTTTTTT ATAGTCCCCG TACCGGGTGA TGCTCTTGGT AGTGGGATTA GTTCAAAAAA	ACGAGAACCA TCACCCCTAAT CAAGTTTTTT TGCTCTTGGT AGTGGGATTA GTTCAAAAAA	TCACCCCTAAT CAAGTTTTTT AGTGGGATTA GTTCAAAAAA
1351	GGGGTCGAGG TGCCCGTAAAG CACTAAATCG GAACCCCTAAA GGGAGCCCCC CCCCAGCTCC ACGGCATTTT GTGATTTAGC CTTGGGATTT CCTCGGGGG	TGCCCGTAAAG CACTAAATCG GAACCCCTAAA GGGAGCCCCC ACGCATTTT GTGATTTAGC CTTGGGATTT CCTCGGGGG	GGAGCCCCC CTTGGGATTT CCTCGGGGG

BanII

~~~~~

FIG. 35A-52

```
1401 GATTTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG AAAGGAAGGG
 CTAATCTCG AACTGCCCTT TTCGGCCGCT TGCACCGCTC TTTCCTTCCC

1451 AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG TAGCGGTCAC
 TTCTTTTCGCT TTCCTCGCCC GCGATCCCGC GACCGTTCAC ATCGCCAGTG

1501 GCTGCGCGTA ACCACCACAC CCGCCGCGCT TAATGCGCCG CTACAGGGCG
 CGACGCGCAT TGGTGGTGTG GCGGCGCGCA ATTACGCGGC GATGTCCCGC

 NheI
      ~~~~~

1551  CGTGCTAGCG GAGTGATATC TGGCTTACTA TGTGGCACT GATGAGGGTG
      GCACGATCGC CTCACATATG ACCGAATGAT ACAACCGTGA CTACTCCCAC

      XmnI
      ~~~~~

1601 TCAGTGAAGT GCTTCATGTG GCAGGAGAAA AAAGGCTGCA CCGGTGCGTC
 AGTCACTTCA CGAAGTACAC CGTCCTCTTT TTTCCGACGT GCCACGCAG

1651 AGCAGAAATAT GTGATACAGG ATATATTCCG CTTCCCTCGCT CACTGACTCG
 TCGTCTTATA CACTATGTCC TATATAAGGC GAAGGAGCGA GTGACTGAGC

1701 CTACGCTCGG TCGTTCGACT GCGGCGAGCG GAAATGGCTT ACGAACGGGG
```

FIG. 35A-53

|      |            |            |            |            |             |
|------|------------|------------|------------|------------|-------------|
|      | GATGCGAGCC | AGCAAGCTGA | CGCCGCTCGC | CTTTACCGAA | TGCTTGCCCC  |
| 1751 | CGGAGATTTC | CTGGAAGATG | CCAGGAAGAT | ACTTAACAGG | GAAGTGAGAG  |
|      | GCCTCTAAAG | GACCTTCTAC | GGTCCTTCTA | TGAATTGTCC | CTTCACTCTC  |
| 1801 | GGCCGCGGCA | AAGCCGTTT  | TCCATAGGCT | CCGCCCCCT  | GACAAGCATC  |
|      | CCGGCGCCGT | TTCCGGCAAA | AGTATCCGA  | GGCGGGGGA  | CTGTTCCGTAG |
| 1851 | ACGAAATCTG | ACGCTCAAAT | CAGTGGTGGC | GAAACCCGAC | AGGACTATAA  |
|      | TGCTTTAGAC | TGCGAGTTA  | GTCACCACCG | CTTTGGGCTG | TCCGTGATATT |
| 1901 | AGATACCAGG | CGTTTCCCC  | TGGCGGCTCC | CTCCTGCGCT | CTCCTGTTCC  |
|      | TCTATGGTCC | GCAAAGGGG  | ACCGCCGAGG | GAGGACGCGA | GAGGACAAAG  |
|      |            | AgeI       | ~~~~~      |            |             |
| 1951 | TGCCTTTTCG | TTTACCGGTG | TCATTCCGCT | GTTATGGCCG | CGTTTGTCTC  |
|      | ACGGAAAGCC | AAATGGCCAC | AGTAAGGCGA | CAATACCGGC | GCAAACAGAG  |
| 2001 | ATTCCACGCC | TGACACTCAG | TTCCGGGTAG | GCAGTTCGCT | CCAAGCTGGA  |
|      | TAAGGTGCGG | ACTGTAGTC  | AAGGCCCATC | CGTCAAGCGA | GGTTCGACCT  |
| 2051 | CTGTATGCAC | GAACCCCCCG | TTCAGTCCGA | CCGCTGCGCC | TTATCCGGTA  |
|      | GACATACGTG | CTTGGGGGGC | AAGTCAGGCT | GGCGACGCGG | AATAGGCCAT  |

FIG. 35A-54

|      |            |            |            |            |            |
|------|------------|------------|------------|------------|------------|
| 2101 | ACTATCGTCT | TGAGTCCAAC | CCGGAAGAC  | ATGCAAAAGC | ACCACTGGCA |
|      | TGATAGCAGA | ACTCAGGTG  | GGCCTTTCTG | TACGTTTTCG | TGGTGACCGT |
| 2151 | GCAGCCACTG | GTAATTGATT | TAGAGGAGTT | AGTCTTGAAG | TCATGCGCCG |
|      | CGTCGGTGAC | CATTAACTAA | ATCTCCTCAA | TCAGAACTTC | AGTACGCGGC |
| 2201 | GTTAAGGCTA | AACTGAAAG  | ACAAGTTTTA | GTGACTGCGC | TCCTCCAAGC |
|      | CAATTCCGAT | TTGACTTTCC | TGTTCAAAAT | CACTGACGCG | AGGAGGTTCC |
| 2251 | CAGTTACCTC | GGTTCAAAGA | GTGGTAGCT  | CAGAGAACCT | ACGAAAACC  |
|      | GTCATGGAG  | CCAAGTTTCT | CAACCATCGA | GTCTCTTGA  | TGCTTTTGG  |
| 2301 | GCCCTGCAAG | GCGGTTTTTT | CGTTTTCAGA | GCAAGAGATT | ACGCGCAGAC |
|      | CGGGACGTTT | CGCCAAAAAA | GCAAAGTCT  | CGTTCTCTAA | TGCGCGTCTG |
| 2351 | CAAAACGATC | TCAAGAAGAT | CATCTTATTA |            |            |
|      | GTTTTGCTAG | AGTTCTTCTA | GTAGAATAAT |            |            |

BglII

FIG. 35A-55



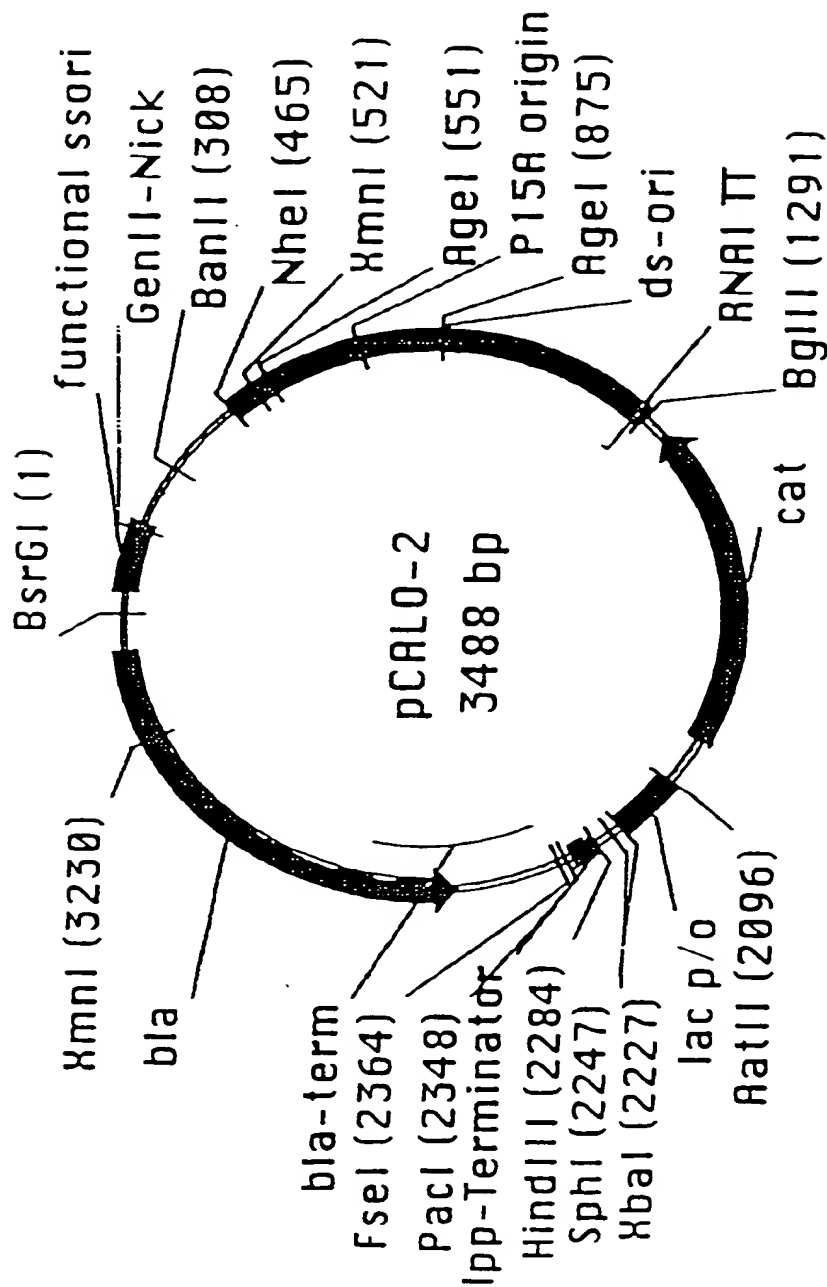


FIG. 35A-56

pCALO-2:

BsrGI

~~~~~

1 GTACATGAAA TTGTAACGTT TAATATTTTG TTAAAATTCG CGTTAAATTT  
CATGTACTTT AACATTTGCA ATTATAAAAC AATTTAAGC GCAATTTAAA

51 TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC  
AACAAATTTAG TCGAGTAATA AATTGGTTAT CCGCCTTAG CCGTTTATAG

101 CTTATAAATC AAAAGAATAG ACCGAGATAG GGTTGAGTGT TGTTCAGTT  
GAATATTTAG TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA

151 TGGACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG TCAAAGGGCG  
ACCTTGTTCT CAGGTGATAA TTTCTTGCAC CTGAGGTTGC AGTTTCCCGC

201 AAAAACCCTC TATCAGGGCG ATGGCCCACT ACGAGAACCA TCACCCTAAT  
TTTTTGGCAG ATAGTCCCGC TACCGGGTGA TGCTCTTGGT AGTGGGATTA

251 CAAGTTTTTT GGGTCCGAGG TGCCGTAAAG CACTAAATCG GAACCCCTAAA  
GTTCAAAAAA CCCCAGCTCC ACGCATTTT GTGATTTAGC CTTGGGATTT

BanII

~~~~~

301 GGGAGCCCCC GATTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG

FIG. 35A-57

```

CCCTCGGGG CTAATCTCG AACTGCCCCCT TTCGGCCGCT TGCACCGCTC

351 AAAGGAAGG AAGAAAGCGA AAGAGCGGG CGTAGGGCG CTGGCAAGTG
TTTCCTTCCC TTCTTTGCT TTCTCGCCC GCGATCCCGC GACCGTTCAC

401 TAGCGGTCAC GCTGCGCGTA ACCACCACAC CCGCCGCGCT TAATGCGCCG
ATCGCCAGTG CGACGCGCAT TGGTGGTGT GCGGCGCGA ATTACGCGGC

 NheI
                                     ~~~~~
451 CTACAGGGCG CGTGCTAGCG GAGTGATAC TGGCTTACTA TGTTGGCACT
GATGTCCCGC GCACGATCGC CTCACATATG ACCGAATGAT ACAACCGTGA

                                     XmnI
                                     ~~~~~
501 GATGAGGGTG TCAGTGAAGT GCTTCATGTG GCAGGAGAAA AAAGGCTGCA
CTACTCCAC AGTCACTTCA CGAAGTACAC CGTCCCTCTTT TTTCCGACGT

AgeI
~~~~~
551 CCGGTGCGTC AGCAGAATAT GTGATACAGG ATATATTCCG CTTCCCTCGCT
GGCCAÇGCAG TCGTCTTATA CACTATGTCC TATATAAGGC GAAGGAGCGA

601 CACTGACTCG CTACGCTCGG TCGTTCGACT GCGGCGAGCG GAAATGGCTT

```

FIG. 35A-58

|     |              |             |             |             |            |
|-----|--------------|-------------|-------------|-------------|------------|
|     | GTGACTGAGC   | GATGCGAGCC  | AGCAAGCTGA  | CGCCGCTCGC  | CTTACCAGAA |
| 651 | ACGAACGGGG   | CGGAGATTTC  | CTGGAAGATG  | CCAGGAAGAT  | ACTTAACAGG |
|     | TGCTTGCCCC   | GCCCTCTAAAG | GACCTTCTAC  | GGTCCTTCTA  | TGAATTGTCC |
| 701 | GAAGTGAGAG   | GGCCGCGGCA  | AAGCCGTTTT  | TCCATAGGCT  | CCGCCCCCCT |
|     | CTTCACTCTC   | CCGGCGCCGT  | TTCGGCAAAA  | AGGTATCCGA  | GGCGGGGGGA |
| 751 | GACAAGCATC   | ACGAAATCTG  | ACGCTCAAAT  | CAGTGGTGGC  | GAAACCCGAC |
|     | CTGTTCTGTAG  | TGCTTTAGAC  | TGCGAGTTTA  | GTCACCCACCG | CTTTGGGCTG |
| 801 | AGGACTATAA   | AGATACCAGG  | CGTTTCCCCC  | TGGCGGCTCC  | CTCCTGCGCT |
|     | TCCTGATATT   | TCTATGGTCC  | GCAAAGGGGG  | ACCGCCGAGG  | GAGACGCCGA |
|     |              |             | AgeI        |             |            |
|     |              |             | ~~~~~       |             |            |
| 851 | CTCCTGTTCC   | TGCCCTTTCCG | TTTACCCGGTG | TCATTCCGCT  | GTTATGGCCG |
|     | GAGGACAAGG   | ACGGAAAGCC  | AAATGGCCAC  | AGTAAGGCCA  | CAATACCCGC |
| 901 | CGTTTGTCCTC  | ATTCCACGCC  | TGACACTCAG  | TTCCGGGTAG  | GCAGTTCGCT |
|     | GCAAACACAGAG | TAAGGTGCGG  | ACTGTGAGTC  | AAGGCCCATC  | CGTCAAGCGA |
| 951 | CCAAGCTGGA   | CTGTATGCAC  | GAACCCCCCG  | TTCAGTCCGA  | CCGCTGCGCC |
|     | GGTTCGACCT   | GACATACGTG  | CTTGGGGGGC  | AAGTACGGCT  | GGCGACGCCG |

FIG. 35A-59

|      |             |            |             |             |             |
|------|-------------|------------|-------------|-------------|-------------|
| 1001 | TTATCCGGTA  | ACTATCGTCT | TGAGTCCAAC  | CCGGAAGAC   | ATGCAAAAGC  |
|      | AATAGGCCAT  | TGATAGCAGA | ACTCAGGTTG  | GGCCTTTCTG  | TACGTTTTCG  |
| 1051 | ACCACCTGGCA | GCAGCCACTG | GTAATTGATT  | TAGAGGAGTT  | AGTCTTTGAAG |
|      | TGGTGACCGT  | CGTCGGTGAC | CATTAACTAA  | ATCTCCTCAA  | TCAGAACTTC  |
| 1101 | TCATGCGCCG  | GTTAAGGCTA | AACTGAAAGG  | ACAAGTTTTA  | GTGACTGCCG  |
|      | AGTACGCGGC  | CAATTCCGAT | TTGACTTTCC  | TGTTCAAAAT  | CACTGACGCG  |
| 1151 | TCCTCCAAGC  | CAGTTACCTC | GGTCAAGA    | GTTGGTAGCT  | CAGAGAACCT  |
|      | AGGAGGTTTC  | GTCAATGGAG | CCAAGTTTCT  | CAACCATCGA  | GTCTCTTGGA  |
| 1201 | ACGAAAACC   | GCCCTGCAAG | GCGGTTTTTT  | CGTTTTCAGA  | GCAAGAGATT  |
|      | TGCTTTTTTG  | CGGACGTTC  | CGCCAAAAAA  | GCAAAAGTCT  | CGTTCTCTAA  |
|      |             |            |             | Bgl II      |             |
|      |             |            |             | ~~~~~       |             |
| 1251 | ACGCGCAGAC  | CAAACGATC  | TCAAGAAGAT  | CATCTTATTA  | GATCTAGCAC  |
|      | TGCGCGTCTG  | GTTTTGCTAG | AGTTCTTCTA  | GTAGAAATAAT | CTAGATCGTG  |
| 1301 | CAGGCGTTTA  | AGGGCACCAA | TAACTGCCCTT | AAAAAAATTA  | CGCCCCGCCC  |
|      | GTCCGCAAAAT | TCCCGTGGTT | ATTGACGGAA  | TTTTTTTAAT  | CGGGGGCGGG  |

FIG. 35A-60

|      |              |             |             |             |             |
|------|--------------|-------------|-------------|-------------|-------------|
| 1351 | TGCCACTCAT   | CGCAGTACTG  | TTGTAATTCA  | TTAAGCATTC  | TGCCGACATG  |
|      | ACGGTGAGTA   | CGGTCATGAC  | AACATTAAAGT | AATTCGTAAG  | ACGGCTGTAC  |
| 1401 | GAAGCCCATCA  | CAAACGGCAT  | GATGAACCTG  | AATCGCCAGC  | GGCATCAGCA  |
|      | CTTCGGTAGT   | GTTTGCCGTA  | CTACTTGGAC  | TTAGCGGTCTG | CCGTAGTCGT  |
| 1451 | CCTTGTCGCC   | TTGCGTATAA  | TATTTGCCCCA | TAGTGAAAAC  | GGGGCGGAAG  |
|      | GAACACGCGG   | AACGCATATT  | ATAAACGGGT  | ATCACTTTTG  | CCCCCGCTTC  |
| 1501 | AAGTTGTCCA   | TATTGGCTAC  | GTTTAAATCA  | AAACTGGTGA  | AACTCACCCA  |
|      | TTCAACACAGGT | ATAACCGATG  | CAAATTTAGT  | TTTGACCACT  | TTGAGTGGGT  |
| 1551 | GGGATTGGCT   | GAGACGAAA   | ACATATTCTC  | AATAAACCCCT | TTAGGGAAAT  |
|      | CCCTAACCGA   | CTCTGCTTTT  | TGTATAAGAG  | TTATTTGGGA  | AATCCCCTTA  |
| 1601 | AGGCCAGGTT   | TTCACCCGTAA | CACGCCACAT  | CTTGCGAATA  | TATGTGTAGA  |
|      | TCCGGTCCAA   | AAGTGGCATT  | GTGCGGTGTA  | GAACGCTTAT  | ATACACATCT  |
| 1651 | AACTGCCCGA   | AATCGTCGTG  | GTATTCACTC  | CAGAGCGATG  | AAAACGTTTC  |
|      | TTGACGGCCT   | TTAGCAGCAC  | CATAAGTGAG  | GTCTCGCTAC  | TTTTTGCAAAG |
| 1701 | AGTTTGCTCA   | TGGAAAACGG  | TGTAACAAGG  | GTGAACACTA  | TCCCATATCA  |
|      | TCAAACGAGT   | ACCTTTTGCC  | ACATTGTTCC  | CACTTGATGAT | AGGTATAGT   |

FIG. 35A-61

|      |             |            |            |             |             |
|------|-------------|------------|------------|-------------|-------------|
| 1751 | CCAGCTCACC  | GTCTTTCATT | GCCATACGGA | ACTCCGGGTG  | AGCATTCATC  |
|      | GGTCGAGTGG  | CAGAAAGTAA | CGGTATGCCT | TGAGGCCCCAC | TCGTAAGTAG  |
| 1801 | AGCGGGGCAA  | GAATGTGAAT | AAAGGCCGGA | TAAAACTTGT  | GCTTATTTTT  |
|      | TCCGCCCGTT  | CTTACACTTA | TTTCCGGCCT | ATTTTGAACA  | CGAATAAAAA  |
| 1851 | CTTTACGGTC  | TTTAAAAAGG | CCGTAATATC | CAGCTGAACG  | GTC TGGTTAT |
|      | GAAATGCCAG  | AAATTTTTC  | GGCATTATAG | GTCGACTTGC  | CAGACCAATA  |
| 1901 | AGGTACATTG  | AGCAACTGAC | TGAAATGCCT | CAAAATGTTC  | TTTACGATGC  |
|      | TCCATGTAAC  | TCGTTGACTG | ACTTTACGGA | GTTTACAAAG  | AAATGCTACG  |
| 1951 | CATTGGGATA  | TATCAACGGT | GGTATATCCA | GTGATTTTTT  | TCTCCATTTT  |
|      | GTAAACCCTAT | ATAGTTGCCA | CCATATAGGT | CACTAAAAAA  | AGAGGTAAAA  |
| 2001 | AGCTTCCCTTA | GCTCCTGAAA | ATCTCGATAA | CTCAAAAAAT  | ACGCCCGGTA  |
|      | TCGAAGGAAT  | CGAGGACTTT | TAGAGCTATT | GAGTTTTTTA  | TGCGGGCCAT  |
|      |             |            |            | AatII       |             |
|      |             |            |            | ~~~~~       |             |
| 2051 | GTGATCTTAT  | TTCATTATGG | TGAAAGTTGG | AACCTCACCC  | GACGTCTAAT  |
|      | CACTAGAATA  | AAGTAATACC | ACTTTCAACC | TTGGAGTGGG  | CTGCAGATTA  |
| 2101 | GTGAGTTAGC  | TCACTCATTA | GGCACCCACG | GCTTTACACT  | TTATGCTTCC  |

FIG. 35A-62

|      |             |            |            |            |            |
|------|-------------|------------|------------|------------|------------|
|      | CACTCAATCG  | AGTGAGTAAT | CCGTGGGGTC | CGAAATGTGA | AATACGAAGG |
| 2151 | GGCTCGTATG  | TTGTGTGGAA | TTGTGAGCGG | ATAACAATTT | CACACAGGAA |
|      | CCGAGCATAC  | AACACACCTT | AACACTCGCC | TATTGTTAAA | GTGTGTCCCT |
|      |             |            | XbaI       |            | SphI       |
|      |             |            | ~~~~~      |            | ~~~~~      |
| 2201 | ACAGCTATGA  | CCATGATTAC | GAATTTCTAG | ACCCCCCCCC | CGCATGCCAT |
|      | TGTCGATACT  | GGTACTAATG | CTTAAAGATC | TGGGGGGGGG | GCGTACGGTA |
|      |             |            |            | HindIII    |            |
|      |             |            |            | ~~~~~      |            |
| 2251 | AAC TTCGTAT | AATGTACGCT | ATACGAAGTT | ATAAGCTTGA | CCTGTGAAGT |
|      | TTGAAGCATA  | TTACATGCGA | TATGCTTCAA | TATTCGAACT | GGACACTTCA |
|      |             |            |            |            | PacI       |
|      |             |            |            |            | ~~~~~      |
| 2301 | GAAAAATGGC  | GCAGATTGTG | CGACATTTT  | TTTGTCTGCC | GTTTAATTAA |
|      | CTTTTACC    | CGCTAACAC  | GCTGTAAAAA | AAACAGACGG | CAAATTAAAT |
|      |             |            |            |            |            |
|      |             |            | FseI       |            |            |
|      |             |            | ~~~~~      |            |            |
| 2351 | GGGGGGGGGC  | CGGCCATTAT | CAAAAAGGAT | CTCAAGAAGA | TCCTTTGATC |
|      | CCCCCCCCCG  | GCCGGTAATA | GTTTTTCCTA | GAGTTCTTCT | AGGAAACTAG |

FIG. 35A-63



|      |            |             |             |             |             |
|------|------------|-------------|-------------|-------------|-------------|
| 2401 | TTTTCTACGG | GGTCTGACGC  | TCAGTGGAAC  | GAAAACTCAC  | GTTAAGGGAT  |
|      | AAAAGATGCC | CCAGACTGCG  | AGTCACCTTG  | CTTTTGAGTG  | CAATTCCCCTA |
| 2451 | TTTGGTCATG | AGATTATCAA  | AAAGGATCTT  | CACCTAGATC  | CTTTTAAATT  |
|      | AAACCAGTAC | TCTAATAGTT  | TTTCCTAGAA  | GTGGATCTAG  | GAAAATTTTAA |
| 2501 | AAAAATGAAG | TTTTAAATCA  | ATCTAAAGTA  | TATATGAGTA  | AACTTGGTCT  |
|      | TTTTTACTTC | AAAATTTAGT  | TAGATTTTCAT | ATATACTCAT  | TTGAACCCAGA |
| 2551 | GACAGTTACC | CAATGCTTAA  | TCAGTGAGGC  | ACCTATCTCA  | GCGATCTGTC  |
|      | CTGTCAATGG | GTTACGGAATT | AGTCACTCCG  | TGGATAGAGT  | CGCTAGACAG  |
| 2601 | TATTTTCGTT | ATCCATAGTT  | GCCTGACTCC  | CCGTCGTGTA  | GATAACTACG  |
|      | ATAAAGCAAG | TAGGTATCAA  | CGGACTGAGG  | GGCAGCACAT  | CTATTGATGC  |
| 2651 | ATACGGGAGG | GCTTACCATC  | TGGCCCCCAGT | GCTGCAATGA  | TACCGCGAGA  |
|      | TATGCCCTCC | CGAATGGTAG  | ACCGGGGTCA  | CGACGTTACT  | ATGGCGCTCT  |
| 2701 | CCCACGCTCA | CCGGCTCCAG  | ATTTATCAGC  | AATAAACCCAG | CCAGCCGGAA  |
|      | GGGTGCGAGT | GGCCGAGGTC  | TAAATAGTCG  | TTATTTGGTC  | GGTCGGCCCTT |
| 2751 | GGGCCGAGCG | CAGAAGTGGT  | CCTGCAACTT  | TATCCGCCCTC | CATCCAGTCT  |
|      | CCCGGCTCGC | GTCTTCACCA  | GGACGTTGAA  | ATAGGCGGAG  | GTAGGTCAGA  |

FIG. 35A-64

|      |              |             |             |            |             |
|------|--------------|-------------|-------------|------------|-------------|
| 2801 | ATTAACGTGT   | GCCGGGAAGC  | TAGAGTAAGT  | AGTTCGCCAG | TTAATAGTTT  |
|      | TAATTGACAA   | CGGCCCTTCG  | ATCTCATTCA  | TCAAGCGGTC | AATTATCAAA  |
| 2851 | GCGCAACGTT   | GTTGCCATTG  | CTACAGGCAT  | CGTGGTGTC  | CGCTCGTCGT  |
|      | CGCGTTGCAA   | CAACGGTAAC  | GATGTCCGTA  | GCACCACAGT | GCGAGCAGCA  |
| 2901 | TTGGTATGGC   | TTCATTTCAGC | TCCGGTTCCC  | AACGATCAAG | GCGAGTTACA  |
|      | AACCATACCG   | AAGTAAGTCG  | AGGCCAAGGG  | TTGCTAGTTC | CGCTCAATGT  |
| 2951 | TGATCCCCCA   | TGTTGTGCAA  | AAAAGCGGTT  | AGCTCCTTCG | GTCCTCCGAT  |
|      | ACTAGGGGGT   | ACAACACGTT  | TTTTTCGCCAA | TCGAGGAAGC | CAGGAGGCTA  |
| 3001 | CGTTGTCAGA   | AGTAAGTTGG  | CCGCAGTGTT  | ATCACTCATG | GTTATGGCAG  |
|      | GCAACAGTCT   | TCATTCAACC  | GGCGTCACAA  | TAGTGAGTAC | CAATACCGTC  |
| 3051 | CAC TG CATAA | TTCTCTTACT  | GTCATGCCAT  | CCGTAAGATG | CTTTTCTGTG  |
|      | GTGACGTATT   | AAGAGAAATGA | CAGTACGGTA  | GGCATTCTAC | GAAAGACAC   |
| 3101 | ACTGGTGAGT   | ACTCAACCAA  | GTCATTCTGA  | GAATAGTGTA | TGCGGCGACC  |
|      | TGACCACTCA   | TGAGTTGGTT  | CAGTAAGACT  | CTTATCACAT | ACGCCGCTGG  |
| 3151 | GAGTTGCTCT   | TGCCCCGGCGT | CAATACGGGA  | TAATACCGCG | CCACATAGCA  |
|      | CTCAACGAGA   | ACGGCCGCA   | GTTATGCCCT  | ATTATGGCGC | GGTGATATCGT |

FIG. 35A-65

XmnI

3201 GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAAC TC  
CTTGAAATTT TCACGAGTAG TAACCTTTTG CAAGAAGCCC CGCTTTTGAG  
3251 TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAA CCACTCGCGC  
AGTTCCCTAGA ATGGCGACAA CTC TAGGTC A GCTACATTG GTGAGCGCG  
3301 ACCCAACTGA TCCTCAGCAT CTTTACTTT CACCAGCGTT TCTGGGTGAG  
TGGGTTGACT AGGAGTCGTA GAAATGAAA GTGTCGCAA AGACCCACTC  
3351 CAAAACACAGG AAGGCAAAAT GCCGCAAAA AGGGAATAAG GCGACACGG  
GTTTTTGTCC TTCCGTTTTA CGCGTTTTT TCCCTTATTC CCGCTGTGCC  
3401 AAATGTTGAA TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA  
TTTACAACCTT ATGAGTATGA GAAGGAAAAA GTTATAATAA CTCGTAAAT

BsrGI

3451 TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAAT  
AGTCCCAATA ACAGAGTACT CGCCTATGTA TAAACTTA

FIG. 35A-66

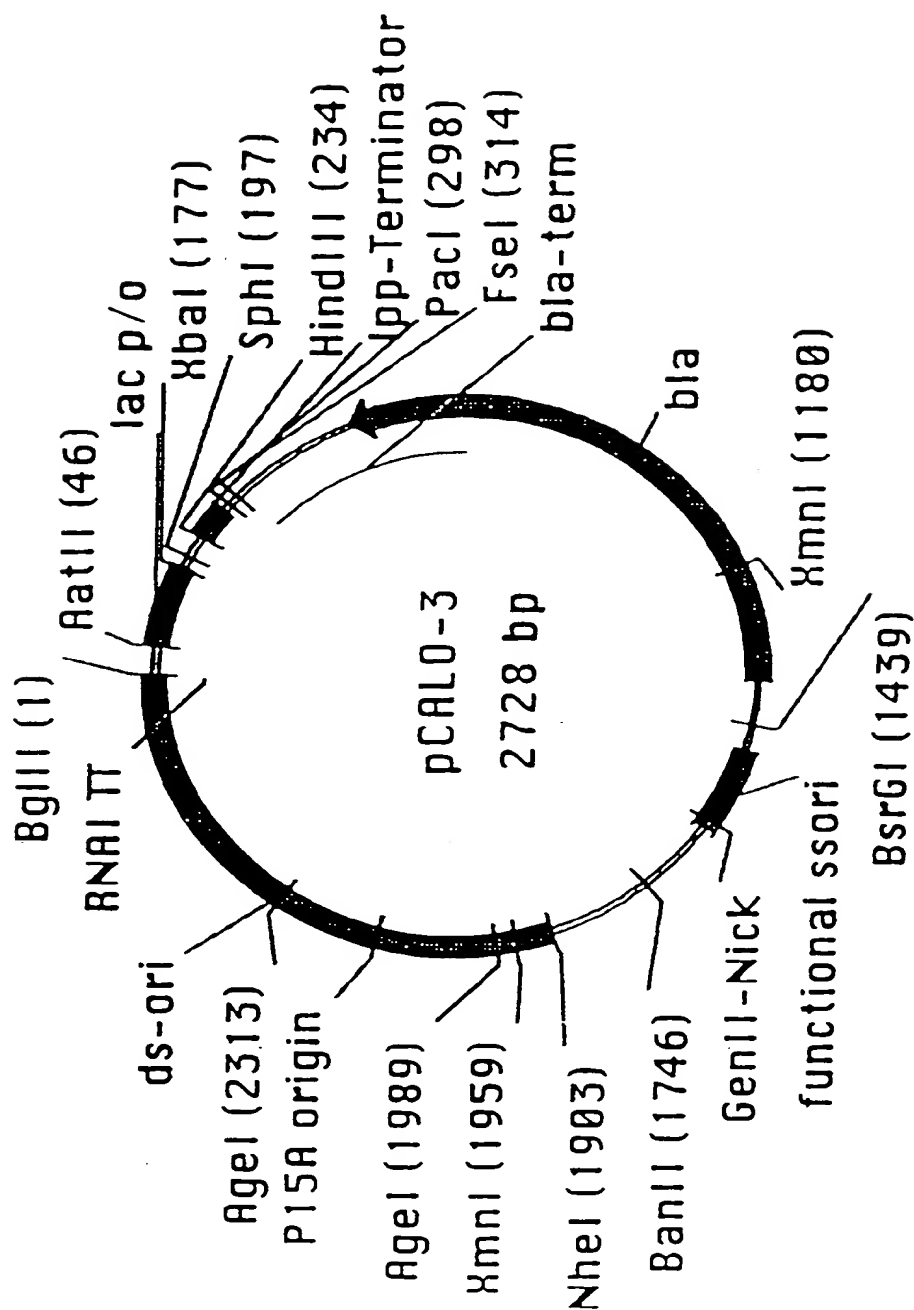


FIG. 35A-67

pCALO-3:

BglII

~~~~~

AatII

~~~~~

1 GATCTCATAA CTTCGTATAA TGTATGCTAT ACGAAGTTAT GACGTCTAAT  
 CTAGAGTATT GAAGCATATT ACATACGATA TGCTTCAATA CTGCAGATTA

51 GTGAGTTAGC TCACTCATTG GGCACCCCGAG GCTTTACACT TTATGCTTCC  
 CACTCAATCG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA AATACGAAGG

101 GGCTCGTATG TTGTGTGGAA TTGTGACGGG ATAACAATTT CACACAGGAA  
 CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCCTT

XbaI

SphI

~~~~~

151 ACAGCTATGA CCATGATTAC GAATTTCTAG ACCCCCCCCC CGCATGCCAT
 TGTCGATACT GGTAATAATG CTTAAAGATC TGGGGGGGGG GCGTACGGTA

HindIII

~~~~~

201 AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA CCTGTGAAGT  
 TTGAAGCATA TTACATGCGA TATGCTTCAA TATTCGAACT GGACACTTCA

PacI

FIG. 35A-68

251 GAAAAATGGC GCAGATTGTG CGACATTTT TTTGTCTGCC GTTAAATTAA  
CTTTTACC CGTCTAACAC GCTGTAAAAA AACAGACGG CAAATTAAAT  
~~~~~

301 GGGGGGGGC CGGCCATTAT CAAAAGGAT CTCAAGAAGA TCCTTTGATC
CCCCCCCCCG GCCGGTAATA GTTTTTCCTA GAGTCTTCT AGGAAACTAG

351 TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT
AAAAGATGCC CCAGACTGCG AGTCACCTTG CTTTGTAGTG CAATTCCCTA

401 TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTAAATT
AAACCAGTAC TCTAATAGTT TTTCCCTAGAA GTGGATCTAG GAAATTTAA

451 AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT
TTTTTACTTC AAAATTTAGT TAGATTTCAT ATATACTCAT TTGAACCCAGA

501 GACAGTTACC CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC
CTGTCAATGG GTTACGAATT AGTCACTCCG TGGATAGAGT CGCTAGACAG

551 TATTTCGTTT ATCCATAGTT GCCTGACTCC CCGTCGTGTA GATAACTACG
ATAAAGCAAG TAGGTATCAA CGGACTGAGG GGCAGCACAT CTATTGATGC

FIG. 35A-69

601 ATACGGGAGG GCTTACCATC TGGCCCCCAGT GCTGCAATGA TACCGCGAGA
TATGCCCTCC CGAATGGTAG ACCGGGTCA CGACGTACT ATGGCGCTCT

651 CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCCAG CCAGCCGGAA
GGTGCGGAGT GGCCGAGGTC TAAATAGTCG TTATTTGGTC GGTCGGCCTT

701 GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCCTC CATCCAGTCT
CCCCGGCTCGC GTCTTCACCA GGACGTTGAA ATAGCGGAG GTAGGTCAGA

751 ATTAACGTGT GCCGGGAAGC TAGAGTAAGT AGTTCGCCCAG TTAATAGTTT
TAATTGACAA CGGCCCTTCG ATCTCATTCA TCAAGCGGTC AATTATCAAA

801 GCGCAACGTT GTTGCCATTG CTACAGGCAT CGTGGTGTC CGCTCGTCGT
CGCGTTGCAA CAACGGTAAC GATGTCCGTA GCACACAGT GCGAGCAGCA

851 TTGGTATGGC TTCATTACGC TCCGGTTCCC AACGATCAAG GCGAGTTACA
AACCATACCG AAGTAAGTCG AGGCCAAGGG TTGCTAGTTC CGCTCAATGT

901 TGATCCCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCCTCCGAT
ACTAGGGGGT ACAACACGTT TTTTCGCCAA TCGAGGAAGC CAGGAGGCTA

951 CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG
GCAACAGTCT TCATTCAACC GGCGTCACAA TAGTGAGTAC CAATACCGTC

FIG. 35A-70

| | | | | | |
|------|-------------|-------------|------------|------------|------------|
| 1001 | CACTGCATAA | TTCTCTTACT | GTCATGCCAT | CCGTAAGATG | CTTTTCTGTG |
| | GTGACGTATT | AAGAGAAATGA | CAGTACGGTA | GGCATTCTAC | GAAAGACAC |
| 1051 | ACTGGTGAGT | ACTCAACCAA | GTCATTCTGA | GAATAGTGTA | TGCGGCGACC |
| | TGACCACTCA | TGAGTTGGTT | CAGTAAGACT | CTATCACAT | ACGCCGCTGG |
| 1101 | GAGTTGCTCT | TGCCCCGGCGT | CAATACGGGA | TAATACCGCG | CCACATAGCA |
| | CTCAACGAGA | ACGGGCCGCA | GTTATGCCCT | ATTATGGCGC | GGTGATCCGT |
| XmnI | | | | | |
| 1151 | GAACTTTAAA | AGTGCTCATC | ATTGGAAAAC | GTTCTTCGGG | GCGAAACTC |
| | CTTGAAATTT | TCACGAGTAG | TAACCTTTTG | CAAGAAGCCC | CGCTTTTGAG |
| 1201 | TCAAGGATCT | TACCGCTGTT | GAGATCCAGT | TCGATGTAAC | CCACTCGCGC |
| | AGTTCCCTAGA | ATGGCGACAA | CTCTAGGTCA | AGCTACATTG | GGTGAGCGCG |
| 1251 | ACCCAACTGA | TCCTCAGCAT | CTTTTACTTT | CACCAGCGTT | TCTGGGTGAG |
| | TGGGTTGACT | AGGAGTCGTA | GAAAATGAAA | GTGGTCGCAA | AGACCCACTC |
| 1301 | CAAAAACAGG | AAGGCAAAAT | GCCGCAAAA | AGGGAATAAG | GCGGACACGG |
| | GTTTTTGTCC | TTCCGTTTTA | CGCGTTTTTT | TCCCTTATTC | CCGCTGTGCC |
| 1351 | AAATGTTGAA | TACTCATACT | CTTCCTTTTT | CAATATTATT | GAAGCATTTA |

FIG. 35A-71

TTTACAACCTT ATGAGTATGA GAAGGAAAAA GTTATAATAA CTTCGTAAAT

BsrGI

~~~~~

1401 TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT ACATGAAATT  
 AGTCCCAATA ACAGAGTACT CGCCTATGTA TAAACTTACA TGTACTTTAA

1451 GTAAACGTTA ATATTTTGTT AAAATTTCGG TTAATTTT GTTAAATCAG  
 CATTGCAAT TATAAAACAA TTTTAAGCGC AATTAAAAA CAATTTAGTC

1501 CTCATTTTTT AACCAATAGG CCGAAATCGG CAAATCCCT TATAAATCAA  
 GAGTAAAAAA TTGGTTATCC GGCTTTAGCC GTTTTAGGGA ATATTTAGTT

1551 AAGAAATAGAC CGAGATAGGG TTGAGTGTG TTCCAGTTG GAACAAGAGT  
 TTCTTATCTG GCTCTATCCC AACTCACAAAC AAGGTCAAAC CTGTTCCTCA

1601 CCACTATTAA AGAACGTGGA CTCCAACGTC AAAGGGCGAA AAACCGTCTA  
 GGTGATAATT TCTTGACCTT GAGGTGCAG TTTCCCCGCTT TTTGGCAGAT

1651 TCAGGGCGAT GGCCCACTAC GAGAACCATC ACCCTAATCA AGTTTTTTGG  
 AGTCCCGCTA CCGGGTGATG CTCCTGGTAG TGGGATTAGT TCAAAAAAAC

BanII

~~~~~

FIG. 35A-72

| | | | | | |
|-------|------------|------------|-------------|-------------|-------------|
| 1701 | GGTCGAGGTG | CCGTAAAGCA | CTAAATCGGA | ACCCTAAAGG | GAGCCCCCGA |
| | CCAGCTCCAC | GGCATTTCGT | GATTTAGCCT | TGGGATTTCC | CTCGGGGGCT |
| 1751 | TTTAGAGCTT | GACGGGGA | GCCGGCGAAC | GTGGCGAGAA | AGGAAGGGAA |
| | AAATCTCGAA | CTGCCCCCTT | CGCGCGCTTG | CACCGCTCTT | TCCTTCCCTT |
| 1801 | GAAAGCGAAA | GGAGCGGGCG | CTAGGGCGCT | GGCAAGTGTA | GCGGTCACGC |
| | CTTTTCGCTT | CCTCGCCCGC | GATCCCGCGA | CCGTTTCACAT | CGCCAGTGCG |
| 1851 | TGCGCGTAAC | CACCACACCC | GCCGGCGCTTA | ATCGCGCGCT | ACAGGGCGCG |
| | ACCGGCATTG | GTGGTGTGGG | CGCGCGGAAT | TACGCGCGGA | TGTCCCGCGC |
| NheI | | | | | |
| ~~~~~ | | | | | |
| 1901 | TGCTAGCGGA | GTGTATACTG | GCTTACTATG | TTGGCACTGA | TGAGGGTGTC |
| | ACGATCGCCT | CACATATGAC | CGAATGATAC | AACCGTGACT | ACTCCCCACAG |
| XmnI | | | | | |
| ~~~~~ | | | | | |
| 1951 | AGTGAAGTGC | TTCATGTGGC | AGGAGAAAAA | AGGCTGCACC | GGTGCGTCAG |
| | TCACTTCACG | AAGTACACCG | TCCTCTTTT | TCCGACGTGG | CCACGCAGTC |
| 2001 | CAGAATATGT | GATACAGGAT | ATATTCCGCT | TCCTCGCTCA | CTGACTCGCT |
| | GTCTTATACA | CTATGTCCTA | TATAAGGCCA | AGGAGCGAGT | GACTGAGCGA |

AgeI

~~~~~

FIG. 35A-73

|       |             |            |             |            |             |
|-------|-------------|------------|-------------|------------|-------------|
| 2051  | ACGCTCGGTC  | GTTCGACTGC | GGCGAGCGGA  | AATGGCTTAC | GAACGGGGCG  |
|       | TGCGAGCCAG  | CAAGCTGACG | CCGCTCGCCT  | TTACCGAATG | CTTGCCCCCG  |
| 2101  | GAGATTTCCCT | GGAAGATGCC | AGGAAGATAC  | TTAACAGGGA | AGTGAGAGGG  |
|       | CTCTAAAGGA  | CCTTCTACGG | TCCTTCTATG  | AATTGTCCCT | TCACTCTCCC  |
| 2151  | CCGCGGCAAA  | GCCGTTTTC  | CATAGGCTCC  | GCCCCCCTGA | CAAGCATCAC  |
|       | GGCGCCGTTT  | CGCAAAAG   | GTATCCGAGG  | CGGGGGACT  | GTTCGTAGTG  |
| 2201  | GAAATCTGAC  | GCTCAAATCA | GTGGTGGCGA  | AACCCGACAG | GACTATAAAG  |
|       | CTTTAGACTG  | CGAGTTTAGT | CACCACCGCT  | TTGGGCTGTC | CTGATATTTC  |
| 2251  | ATACCAGGCG  | TTTCCCCCTG | GCGGCTCCCT  | CCTGCGCTCT | CCTGTTCCCTG |
|       | TATGGTCCGC  | AAAGGGGGAC | CGCCGAGGGA  | GGACGCGAGA | GGACAAGGAC  |
| AgeI  |             |            |             |            |             |
| ~~~~~ |             |            |             |            |             |
| 2301  | CCTTTCGGTT  | TACCGGTGTC | ATTCGGCTGT  | TATGGCCGCG | TTTGTCTCAT  |
|       | GAAAGCCAA   | ATGGCCACAG | TAAGGCGACA  | ATACCGGCGC | AAACAGAGTA  |
| 2351  | TCCACGCCCTG | ACACTCAGTT | CCGGGTAGGC  | AGTTCGCTCC | AAGCTGGACT  |
|       | AGGTGCGGAC  | TGTGAGTCAA | GGCCCCATCCG | TCAAGCGAGG | TTCGACCTGA  |

FIG. 35A-74

|      |            |             |             |             |             |
|------|------------|-------------|-------------|-------------|-------------|
| 2401 | GTATGCACGA | ACCCCCCGTT  | CAGTCCGACC  | GCTGCGCCCTT | ATCCGGTAAC  |
|      | CATACGTGCT | TGGGGGGCAA  | GTCAGGCTGG  | CGACGCCGAA  | TAGGCCATTG  |
| 2451 | TATCGTCTTG | AGTCCAACCC  | GGAAAGACAT  | GCAAAAGCAC  | CACTGGCAGC  |
|      | ATAGCAGAAC | TCAGGTGGG   | CCTTTCGTGTA | CGTTTTCGTG  | GTGACCCGTCG |
| 2501 | AGCCACTGGT | AATTGATTTA  | GAGAGTTAG   | TCTTGAAGTC  | ATGCGCCGGT  |
|      | TCGGTGACCA | TTAACTAAAT  | CTCCTCAATC  | AGAACTTCAG  | TACGCGGCCA  |
| 2551 | TAAGGCTAAA | CTGAAAGGAC  | AAGTTTTAGT  | GACTGCGCTC  | CTCCAAGCCA  |
|      | ATTCCGATTT | GACTTTCCTG  | TTCAAAATCA  | CTGACGCGAG  | GAGGTTCCGT  |
| 2601 | GTTACCTCGG | TTCAAAGAGT  | TGGTAGCTCA  | GAGAACCTAC  | GAAAAACCGC  |
|      | CAATGGAGCC | AAGTTTCTCA  | ACCATCGAGT  | CTCTTGATG   | CTTTTGGCG   |
| 2651 | CCTGCAAGGC | GGTTTTTTTCG | TTTTCAGAGC  | AAGAGATTAC  | GCGCAGACCA  |
|      | GGACGTTCCG | CCAAAAAAGC  | AAAAGTCTCG  | TTCTCTAATG  | CGCGTCTGGT  |

# BglII

|      |            |            |          |
|------|------------|------------|----------|
| 2701 | AAACGATCTC | AAGAAGATCA | TCTTATTA |
|      | TTTGCTAGAG | TTCTTCTAGT | AGAATAAT |

FIG. 35A-75

M1: PCR using template

NoVspAatII: TAGACGTC

M2: synthesis

BloxA-A: TATGAGATCTCATAACTTCGTATAATGTACGCTATACG-  
AAGTTAT

BloxA-B: TAATAACTTCGTATAGCATACATTATACGAAGTTATG-  
AGATCTCA

M3: PCR, NoVspAatII as second oligo

XloxS-muta: CATTTTTGCCCTCGTTATCTACGCATGCGATAACTTCGTA-  
TAGCGTACATTATACGAAGTTATTCTAGACATGGTCATAGCTGTTTCCTG

M7-I: PCR

gIIINEW-fow: GGGGGGAATTCGGTGGTGGTGGATCTGCGTGCGCTG-  
AAACGGTTGAAAGTTG

gIIINEW-rev: CCCCCCAAGCTTATCAAGACTCCTTATTACG

M7-II: PCR

gIIIss-fow: GGGGGGGGAATTCGGAGGCGGTCCGGTGGTGGC

M7-III: PCR

gIIIsupernew-fow: GGGGGGGGAATTCGAGCAGAAGCTGATCTCT-  
GAGGAGGATCTGTAGGGTGGTGGCTCTGGTCCGGTGATTTG

**FIG. 35A-76**

M8: synthesis

lox514-A: CCATAACTTCGTATAATGTACGCTATACGAAGTTATA

lox514-B: AGCTTATAACTTCGTATAGCGTACATTATACGAAGT-  
TATGGCATG

M9II: synthesis

M9II-fow: AGCTTGACCTGTGAAGTGAAAAATGGCGCAGATT-  
GTGCGACATTTTTTTGTCTGCCGTTTAATTAAAGGGGGGGT

M9II-rev: GTACACCCCCCCCCAGGCCGGCCCCCCCCCCCCCTTTAA-  
TTAAACGGCAGACAAAAAAAATGTCGCACAATCTGCG

M10II: assembly PCR with template

bla-fow: GGGGGGGTGTACATTCAAATATGTATCCGCTCATG

bla-seq4: GGGTTACATCGAACTGGATCTC

bla1-muta: CCAGTTCGATGTAACCCACTCGCGCACCCAACTGATC-  
CTCAGCATCTTTACTTTCACC

blaII-muta: ACTCTAGCTTCCCGGCAACAGTTAATAGACTGGATG-  
GAGGCGG

bla-NEW: CTGTTGCCGGGAAGCTAGAGTAAG

bla-rev: CCCCCCTTAATTAAGGGGGGGGGCCGGCCATTATCAAA-  
AAGGATCTCAAGAAGATCC

M11II/III: PCR, site-directed mutagenesis

FIG. 35A-77

f1-fow: GGGGGGGGCTAGCACGCGCCCTGTAGCGGCGCATTA

f1-rev: CCCCCCTGTACATGAAATTGTAAACGTTAATATTTG

f1-t133.muta: GGGCGATGGCCCACTACGAGAACCATCACCTAATC

M12: assembly PCR using template

p15-fow: GGGGGGAGATCTAATAAGATGATCTTCTTGAG

p15-NEWI: GAGTTGGTAGCTCAGAGAACCTACGAAAAACCGCCCTG-  
CAAGGCG

p15-NEWII: GTAGGTTCTCTGAGCTACCAACTC

p15-NEWIII: GTTCCCCCTGGCGGCTCCCTCCTGCGCTCTCCTGTTCT-  
GCC

p15-NEWIV: AGGAGGGAGCCGCCAGGGGGGAAAC

p15-rev: GACATCAGCGCTAGCGGAGTGTATAC

M13: synthesis

BloxXB-A: GATCTCATAACTTCGTATAATGTATGCTATACGAAGTTA-  
TTCA

BloxXB-B: GATCTGAATAACTTCGTATAGCATAATTATACGAAGTTA-  
TGAGA

M14-Ext2: PCR, site-directed mutagenesis

ColEXT2-fow: GGGGGGGGAGATCTGACCAAAATCCCTTAACGTGAG

Col-mutal: GGTATCTGCGCTCTGCTGTAGCCAGTTACCTTCGG

FIG. 35A-78

Col-rev: CCCCCCGCTAGCCATGTGAGCAAAAGGCCAGCAA

M17: assembly PCR using template

CAT-1: GGGACGTCGGGTGAGGTTCCAAC

CAT-2: CCATACGGAACCTCCGGGTGAGCATTCATC

CAT-3: CCGGAGTTCCGTATGG

CAT-4: ACGTTTAAATCAAACTGG

CAT-5: CCAGTTTTGATTAAACGTAGCCAATATGGACAACCTTCTTC-  
GCCCCCGTTTTCACTATGGGCAAATATT

CAT-6: GGAAGATCTAGCACCAGGCGTTTAAG

M41: assembly PCR using template

LAC1: GAGGCCGGCCATCGAATGGCGCAAAAC

LAC2: CGCGTACCGTCCTCATGGGAGAAAATAATAC

LAC3: CCATGAGGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCA-  
TTGGGTCACCAGCAAATCCGCTGTTAGCTGGCCCATTAAG

LAC4: GTCAGCGGCGGGATATAACATGAGCTGTCCTCGGTATCGTCG

LAC5: GTTATATCCCGCCGCTGACCACCATCAAAC

LAC6: CATCAGTGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGT4TTG-  
GGAGCCAGGGTGGTTTTTC

LAC7: GGTTAATTAACCTCACTGCCCCGCTTTCAGTCGGGAAACCTGTCGTGCC-  
AGCTGCATCAGTGAATCGGCCAAC

M41-MCS-fow: CTAGACTAGTGTTTAAACCGGACCGGGGGGGGGGCTT-  
AAGGGGGGGGGGGGGG

**FIG. 35A-79**



M41-MCS-rev: CTAGCCCCCCCCCCCCCTTAAGCCCCCCCCCGGTCCGGT-  
TTAAACACTAGT

M41-fow: CTAGACTAGTGTTTAAACCGGACCGGGGGGGGGCTTAA-  
GGGGGGGGGGGG

M41-rev: CCCCCCTTAAGTGGGCTGCAAAACAAAACGGCCTCC-  
TGTCAGGAAGCCGCTTTTATCGGGTAGCCTCACTGCCCCGCTTCC

M41-A2: GTTGTTGTGCCACGCGGTTAGGAATGTAATTCAGCTCCGC

M41-B1: AACCGCGTGGCACAACAAC

M41-B2: CTCGTTCTACCATCGACACGACCACGCTGGCACCCAGTTG

M41-C1: GTGTCGATGGTAGAACGAAG

M41-CII: CCACAGCAATAGCATCCTGGTCATCCAGCGGATAGTT-  
AATAATCAGCCCACTGACACGTTGCGCGAG

M41-DI: GACCAGGATGCTATTGCTGTGG

M41-DII: CAGCGCGATTGCTGGTGGCCCAATGCGACCAGATGC

M41-EI: CACCAGCAAATCGCGCTG

M41-EII: CCCGGACTCGGTAATGGCACGCATTGCGCCCAGCGCC

M41-FI: GCCATTACCGAGTCCGGG

M42: synthesis

Eco-H5-Hind-fow: AATTCCACCATCATCACCATTGACGTCTA

Eco-H5-Hind-rev: AGCTTAGACGTCAATGGTGATGATGGTGG

FIG. 35A-80